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(71) **Applicant (for all designated States except US): GENENTECH, INC.** [US/US]; 1 DNA Way, South San Francisco, CA 94080-4990 (US).

(72) **Inventors; and**

(75) **Inventors/Applicants (for US only): BAKER, Kevin, P.** [GB/US]; 14006 Indian Run Drive, Darnestown, MD 20878 (US). **DESNOYERS, Luc** [CA/US]; 2050 Stockton Street, San Francisco, CA 94133 (US). **GERRITSEN, Mary, E.** [CA/US]; 541 Parrott Drive, San Mateo, CA 94402 (US). **GODDARD, Audrey** [CA/US]; 110 Congo Street, San Francisco, CA 94131 (US). **GODOWSKI, Paul, J.** [US/US]; 2627 Easton Drive, Burlingame, CA 94010 (US). **GRIMALDI, J., Christopher** [US/US]; 1434 36th Avenue, San Francisco, CA 94122 (US). **GURNEY, Austin, L.** [US/US]; 1 Debbie Lane, Belmont, CA 94002 (US). **SMITH, Victoria** [AU/US]; 19 Dwight Road, Burlingame, CA 94010 (US). **STEPHAN, Jean-Philippe, F.** [FR/US]; 320 C Lansdale Avenue, Millbrae, CA 94030 (US). **WATANABE, Colin, K.** [US/US]; 128 Corliss Drive, Moraga, CA 94556 (US). **WOOD, William, I.** [US/US]; 35 Southdown Court, Hillsborough, CA 94010 (US).

(74) **Agents: BARNES, Elizabeth, M. et al.;** c/o Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).

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# SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

## FIELD OF THE INVENTION

5 The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

## BACKGROUND OF THE INVENTION

10 Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of  
15 action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts  
20 are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci. 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation,  
25 differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins.  
30 Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

#### SUMMARY OF THE INVENTION

In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%



5 nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

10 In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80 % nucleic acid sequence identity, alternatively at least about 81 % nucleic acid sequence identity, alternatively at least about 82 % nucleic acid sequence identity, alternatively at least about 83 % nucleic acid sequence identity, alternatively at least about 84 % nucleic acid sequence identity, alternatively at least about 85 % nucleic acid sequence identity, alternatively at least about 86 % nucleic acid sequence identity, alternatively at least about 87 % nucleic acid sequence identity, alternatively at least about 88 % nucleic acid sequence identity, alternatively at least about 89 % nucleic acid sequence identity, alternatively at least about 90 % nucleic acid sequence identity, alternatively at least about 91 % nucleic acid sequence identity, alternatively at least about 92 % nucleic acid sequence identity, alternatively at least about 93 % nucleic acid sequence identity, alternatively at least about 94 % nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

20 Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

25 Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

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amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1B show a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO6004 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA92259".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figures 1A-1B.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO4981 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA94849-2960".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO7174 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA96883-2745".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO5778 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA96894-2675".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO4332 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA100272-2969".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO9799 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA108696-2966".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

5 Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO9909 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA117935-2801".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO9917 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA119474-2803".

10 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO9771 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA119498-2965".

15 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO9877 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA119502-2789".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

20 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO9903 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA119516-2797".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

25 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO9830 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA119530-2968".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO7155 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA121772-2741".

30 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO9862 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA125148-2782".

35 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO9882 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA125150-2793".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO9864 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA125151-2784".

5 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO10013 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA125181-2804".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

10 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO9885 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA125192-2794".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

15 Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO9879 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA125196-2792".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO10111 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA125200-2810".

20 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO9925 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA125214-2814".

25 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO9905 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA125219-2799".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

30 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO10276 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA128309-2825".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

35 Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO9898 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA129535-2796".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO9904 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA129549-2798".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

5 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO19632 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA129580-2863".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO19672 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA129794-2967".

10 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO9783 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA131590-2962".

15 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO10112 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA135173-2811".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

20 Figures 59A-59B show a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO10284 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA138039-2828".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figures 59A-59B.

25 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO10100 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA139540-2807".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO19628 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA139602-2859".

30 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO19684 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA139632-2880".

35 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO10274 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA139686-2823".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO9907 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA142392-2800".

5 Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO9873 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA143076-2787".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

10 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO10201 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA143294-2818".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

15 Figure 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO10200 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA143514-2817".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO10196 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA144841-2816".

20 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO10282 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA148380-2827".

25 Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO19650 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA149995-2871".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

30 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO21184 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA167678-2963".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

35 Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO21201 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA168028-2956".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.



Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO21175 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA173894-2947".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

5 Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO21340 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA176775-2957".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO21384 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA177313-2982".

10 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO982 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA57700-1408".

15 Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO1160 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA62872-1509".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

20 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1187 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA62876-1517".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

25 Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA66660-1585".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO231 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA34434-1139".

30 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO357 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA44804-1248".

35 Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO725 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA52758-1399".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA59849-1504".

5 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1306 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA65410-1569".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

10 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA71290-1630".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

15 Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO229 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA33100-1159".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1272 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA64896-1539".

20 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO4405 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA84920-2614".

25 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO181 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA23330-1390".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

30 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO214 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA32286-1191".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

35 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO247 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA35673-1201".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO337 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA43316-1237".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

5 Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO526 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA44184-1319".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO363 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA45419-1252".

10 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO531 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA48314-1320".

15 Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1083 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA50921-1458".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

20 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO840 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA53987".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

25 Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1080 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56047-1456".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO788 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56405-1357".

30 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56531-1648".

35 Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56865-1491".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO826 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA57694-1341".

5 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1005 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA57708-1411".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

10 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO809 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA57836-1338".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

15 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA57841-1522".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA58847-1383".

20 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA59212-1627".

25 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO1309 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA59588-1571".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

30 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1025 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA59622-1334".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

35 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1181 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA59847-2510".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1126 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA60615-1483".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1186 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA60621-1516".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1192 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA62814-1521".

Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1244 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA64883-1526".

Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1274 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA64889-1541".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1412 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA64897-1628".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1286 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA64903-1553".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1330 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA64907-1163-1".

Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1347 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA64950-1590".

Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA64952-1568".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1273 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA65402-1540".

5 Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1279 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA65405-1547".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

10 Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1340 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA66663-1598".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

15 Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1338 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA66667".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA66675-1587".

20 Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1376 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA67300-1605".

25 Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1387 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA68872-1620".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

30 Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA71269-1621".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

35 Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1488 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA73736-1657".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

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Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1474 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA73739-1645".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

5 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1917 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA76400-2528".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA76532-1702".

10 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA76541-1675".

15 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1887 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA79862-2522".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

20 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA81754-2532".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

25 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO4341 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA81761-2583".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO5723 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA82361".

30 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA83500-2506".

35 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA84210-2576".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO3543 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA86571-2551".

5 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO3444 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA87997".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

10 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO4302 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA92218-2554".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

15 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO4322 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA92223-2567".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO5725 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA92265-2669".

20 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO4408 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA92274-2617".

25 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO9940 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA92282".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

30 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO7154 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA108760-2740".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

35 Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO7425 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA108792-2753".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.



Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO6079 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA111750-2706".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

5 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO9836 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA119514-2772".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO10096 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA125185-2806".

10 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

#### I. Definitions

15 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein  
20 may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO  
25 polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g.,  
30 an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in  
35 bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino

acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1 % of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5 % of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid

sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X," "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

5 "PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed  
10 herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid  
15 sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95%  
20 nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or  
25 without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180  
30 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences  
35 identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent

nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against

which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated

polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature.

5 Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

10 The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

15 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and  
20 in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below).  
25 The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and  
30 generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired  
35 homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).



"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that:

- (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')<sub>2</sub>, and Fv fragments; diabodies; linear antibodies (Zapata et al., *Protein Eng.* 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')<sub>2</sub> fragment that has two antigen-combining sites and is still

capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the  $V_H$ - $V_L$  dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group.  $F(ab')_2$  antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the  $V_H$  and  $V_L$  domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the  $V_H$  and  $V_L$  domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) in the same polypeptide chain ( $V_H$ - $V_L$ ). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing

conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

5 An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

10 By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a  
15 discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

20 A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

**Table 1**

```

/*
*
* C-C increased from 12 to 15
* Z is average of EQ
5  * B is average of ND
* match with stop is _M; stop-stop = 0; J (joker) match = 0
*/
#define _M      -8      /* value of a match with a stop */

10 int _day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

40

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT         3      /* value of matching bases */
#define DMIS         0      /* penalty for mismatched bases */
#define DINS0        8      /* penalty for a gap */
15
#define DINS1         1      /* penalty per base */
#define PINS0         8      /* penalty for a gap */
#define PINS1         4      /* penalty per residue */

struct jmp {
20
    short            n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short   x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
25
    int              score;      /* score at last jmp */
    long             offset;     /* offset of prev block */
    short            jmp;        /* current jmp index */
    struct jmp        jp;        /* list of jmps */
};

30
struct path {
    int              spc;        /* number of leading spaces */
    short            n[JMPS]; /* size of jmp (gap) */
    int              x[JMPS]; /* loc of jmp (last elem before gap) */
35
};

char              *ofile;      /* output file name */
char              *name[2];    /* seq names: getseqs() */
char              *prog;       /* prog name for err msgs */
40
char              *seq[2];     /* seqs: getseqs() */
int               dmax;        /* best diag: nw() */
int               dmax0;       /* final diag */
int               dna;         /* set if dna: main() */
int               endgaps;     /* set if penalizing end gaps */
45
int               gapx, gapy;   /* total gaps in seqs */
int               len0, len1;   /* seq lens */
int               ngapx, ngapy; /* total size of gaps */
int               smax;        /* max score: nw() */
int               *xbm;        /* bitmap for matching */
50
long              offset;      /* current offset in jmp file */
struct            diag         /* holds diagonals */
struct            path         /* holds path for seqs */
{
    *calloc(), *malloc(), *index(), *strcpy();
55
    *getseq(), *g_calloc();
}

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
*   where file1 and file2 are two dna or two protein sequences.
5  * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
15 #include "nw.h"
#include "day.h"

static _dbval[26] = {
    1, 14, 2, 13, 0, 0, 4, 11, 0, 0, 12, 0, 3, 15, 0, 0, 0, 5, 6, 8, 8, 7, 9, 0, 10, 0
};
20 static _pbval[26] = {
    1, 2 | (1 < (<('D'-'A')) | (1 < (<('N'-'A'))), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1 < < 10, 1 < < 11, 1 < < 12, 1 < < 13, 1 < < 14,
    1 < < 15, 1 < < 16, 1 < < 17, 1 < < 18, 1 < < 19, 1 < < 20, 1 < < 21, 1 < < 22,
25 1 < < 23, 1 < < 24, 1 < < 25 | (1 < (<('E'-'A')) | (1 < (<('Q'-'A'))
};

main(ac, av)                                main
    int    ac;
    char   *av[];
30 {
    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                                /* 1 to penalize endgaps */
    ofile = "align.out";                        /* output file */

50     nw();                                    /* fill in the matrix, get the possible jmps */
    readjmps();                                /* get the actual jmps */
    print();                                    /* print stats, alignment */

55     cleanup();                                /* unlink any tmp files */
}

```

**Table 1 (cont')**

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
{
    char *      *px, *py;      /* seqs and ptrs */
    int         *ndely, *dely; /* keep track of dely */
    int         ndelx, delx;    /* keep track of delx */
    int         *tmp;          /* for swapping row0, row1 */
    int         mis;           /* score for each type */
    int         ins0, ins1;     /* insertion penalties */
    register    id;            /* diagonal index */
    register    ij;            /* jmp index */
    register    *col0, *col1;   /* score for curr, last row */
    register    xx, yy;         /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0; /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
    */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```



Table 1 (c nt')

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
  mis = col0[yy-1];
  if (dna)
    mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
  else
    mis += _day[*px-'A'][*py-'A'];

  /* update penalty for del in x seq;
   * favor new del over ongong del
   * ignore MAXGAP if weighting endgaps
   */
  if (endgaps || ndely[yy] < MAXGAP) {
    if (col0[yy] - ins0 >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else {
      dely[yy] -= ins1;
      ndely[yy]++;
    }
  } else {
    if (col0[yy] - (ins0+ins1) >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else
      ndely[yy]++;
  }

  /* update penalty for del in y seq;
   * favor new del over ongong del
   */
  if (endgaps || ndelx < MAXGAP) {
    if (col1[yy-1] - ins0 >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else {
      delx -= ins1;
      ndelx++;
    }
  } else {
    if (col1[yy-1] - (ins0+ins1) >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else
      ndelx++;
  }

  /* pick the maximum score; we're favoring
   * mis over any del and delx over dely
   */

```

Table 1 (cont')

...nw

```

5      id = xx - yy + len1 - 1;
      if (mis >= delx && mis >= dely[yy])
          coll[yy] = mis;
      else if (delx >= dely[yy]) {
10         coll[yy] = delx;
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
          && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
15             dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
                  offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = ndelx;
          dx[id].jp.x[ij] = xx;
          dx[id].score = delx;
20      }
      else {
          coll[yy] = dely[yy];
          ij = dx[id].ijmp;
25      if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
          && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
          dx[id].ijmp++;
          if (++ij >= MAXJMP) {
30              writejumps(id);
              ij = dx[id].ijmp = 0;
              dx[id].offset = offset;
              offset += sizeof(struct jmp) + sizeof(offset);
          }
      }
          dx[id].jp.n[ij] = -ndely[yy];
          dx[id].jp.x[ij] = xx;
          dx[id].score = dely[yy];
35      }
      if (xx == len0 && yy < len1) {
          /* last col
          */
          if (endgaps)
              coll[yy] -= ins0+ins1*(len1-yy);
          if (coll[yy] > smax) {
45              smax = coll[yy];
              dmax = id;
          }
      }
  }
50      if (endgaps && xx < len0)
          coll[yy-1] -= ins0+ins1*(len0-xx);
      if (coll[yy-1] > smax) {
          smax = coll[yy-1];
          dmax = id;
55      }
      tmp = col0; col0 = coll; coll = tmp;
  }
  (void) free((char *)ndely);
  (void) free((char *)dely);
60  (void) free((char *)col0);
  (void) free((char *)coll);
  }

```

Table 1 (c nt')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3 /* space between name or num and seq */

20 extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25 print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "< first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "< second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
50         lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
55         lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

60

```

print

Table 1 (cont')

getmat

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)
    int    lx, ly;          /* "core" (minus endgaps) */
    int    firstgap, lastgap; /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
10    char     outx[32];
    double   pct;
    register n0, n1;
    register char *p0, *p1;

15    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
20    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
25         if (siz0) {
             p1++;
             n1++;
             siz0--;
         }
         else if (siz1) {
30             p0++;
             n0++;
             siz1--;
         }
         else {
35             if (xbm[*p0-'A']&xbm[*p1-'A'])
                 nm++;
             if (n0++ == pp[0].x[i0])
40                 siz0 = pp[0].n[i0++];
             if (n1++ == pp[1].x[i1])
                 siz1 = pp[1].n[i1++];
             p0++;
             p1++;
         }
45     }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
50    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
55    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
60

```

**Table 1 (cont')**

...getmat

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapx, (dna)? "base": "residue", (ngapx == 1)? "": "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, "(%d %s%s)",
            ngapy, (dna)? "base": "residue", (ngapy == 1)? "": "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINSO, DINS1);
    else
        fprintf(fx,
            "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINSO, PINS1);
    if (endgaps)
        fprintf(fx,
            "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base": "residue", (firstgap == 1)? "": "s",
            lastgap, (dna)? "base": "residue", (lastgap == 1)? "": "s");
    else
        fprintf(fx, "< endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(nameex[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

pr\_align

**Table 1 (cont')**

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
5         * do we have more of this sequence?
        */
        if (!*ps[i])
            continue;

10        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
15        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
20        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
25            po[i]++;
            ps[i]++;

            /*
30            * are we at next gap for this seq?
            */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
35                * we need to merge all gaps
                * at this location
                */
                siz[i] = pp[i].n[ij[i] + +];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i] + +];
40                }
                ni[i]++;
            }
        }
        if (++nn == olen || !more && nn) {
45            dumpblock();
            for (i = 0; i < 2; i++)
                po[i] = out[i];
            nn = 0;
        }
50    }

    /*
    * dump a block of lines, including numbers, stars: pr_align()
    */
55    static
    dumpblock()
    {
        register i;

60        for (i = 0; i < 2; i++)
            *po[i]-- = '\0';
    }
}

```

...pr\_align

dumpblock

Table 1 (c nt')

...dumpblock

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10         putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15         }
      }

/*
20  * put out a number line: dumpblock()
  */
  static
  nums(ix)
25  {
      int      ix;      /* index in out[] holding seq line */
      char      nline[P_LINE];
      register  i, j;
      register char *pn, *px, *py;

30      for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
          *pn = ' ';
      for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
          if (*py == ' ' || *py == '-')
              *pn = ' ';
35          else {
              if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                  j = (i < 0)? -i : i;
                  for (px = pn; j /= 10, px--)
                      *px = j%10 + '0';
40                  if (i < 0)
                      *px = '-';

                  }
              else
45                  *pn = ' ';
                  i++;
              }
          }
      *pn = '\0';
      nc[ix] = i;
50      for (pn = nline; *pn; pn++)
          (void) putc(*pn, fx);
      (void) putc('\n', fx);
  }

55  /*
  * put out a line (name, [num], seq, [num]): dumpblock()
  */
  static
  putline(ix)
60      int      ix;      {

```

nums

putline

Table 1 (cont')

...putline

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
10         (void) putc(' ', fx);

      /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
  static
25  stars()
  {
      int          i;
      register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
          return;
      px = star;
35     for (i = lmax+P_SPC; i; i--)
          *px++ = ' ';

      for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
          if (isalpha(*p0) && isalpha(*p1)) {
40             if (xbm[*p0-'A']&xbm[*p1-'A']) {
                 cx = '*';
                 nm++;
             }
45             else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                 cx = '.';
             else
                 cx = ' ';
          }
          else
50             cx = ' ';
          *px++ = cx;
      }
      *px++ = '\n';
      *px = '\0';
55  }

```

stars

60



Table 1 (c nt')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;
10     py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
15     if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
20
```

**Table 1 (cont')**

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

10 char *jname = "/tmp/homgXXXXXX"; /* tmp file for jumps */
FILE *fj;

int cleanup(); /* cleanup tmp file */
15 long lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)
    int i;
{
    if (fj)
        (void) unlink(jname);
25     exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30 char *
getseq(file, len)
35 char *file; /* file name */
    int *len; /* seq len */
{
    char line[1024], *pseq;
    register char *px, *py;
    int natgc, tlen;
    FILE *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

cleanup

getseq

Table 1 (cont')

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);
5
while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
15            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
20    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

25 char *
g_alloc(msg, nx, sz)
    char *msg;          /* program, calling routine */
    int nx, sz;          /* number and size of elements */
{
30     char *px, *calloc;

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
35             fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
40 }

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
45 {
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

50     if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
55         }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
        while (1) {
60             for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)

```

g\_call c

readjmps

**Table 1 (cont')****...readjumps**

```

5      if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
      }
      else
10         break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
             */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
30        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
40        }
    }
    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
60        offset = 0;
    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)
    int    ix;
    {
        char    *mktemp();
10         if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15         if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
20         (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }
}

```

**writejumps**

25

30

35

40

45

50

55

60

**Table 2**

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYY	(Length = 12 amino acids)

5      % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10      5 divided by 15 = 33.3%

**Table 3**

PRO	XXXXXXXXXX	(Length = 10 amino acids)
15      Comparison Protein	XXXXXXXXYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

20      (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

**Table 4**

25      PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

35

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLLVV	(Length = 9 nucleotides)

5     % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10     4 divided by 12 = 33.3%

## II.            Compositions and Methods of the Invention

### A.            Full-Length PRO Polypeptides

15     The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein  
20     as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the  
25     nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

### B.            PRO Polypeptide Variants

30     In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

35     Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by  
5 comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by  
10 systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO  
15 polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired  
20 fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading  
25 of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.



Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
20	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
25	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	
		ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;  
 (2) neutral hydrophilic: cys, ser, thr;  
 (3) acidic: asp, glu;  
 (4) basic: asn, gln, his, lys, arg;  
 (5) residues that influence chain orientation: gly, pro; and  
 40 (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

### C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an  $\alpha$ -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

#### D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

##### 1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like <sup>32</sup>P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

## 2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example,  $\text{CaCl}_2$ ,  $\text{CaPO}_4$ , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC

55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan<sup>r</sup>*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan<sup>r</sup>*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al.,  
10 J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilae* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces*  
15 such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not  
20 limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant  
25 cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138,  
30 ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

### 3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector  
35 for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

5           The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces*  $\alpha$ -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as  
10           signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

15           Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the  $2\mu$  plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for  
20           cloning vectors in mammalian cells.

          Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

25           An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979);  
30           Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

          Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well  
35           known. Promoters suitable for use with prokaryotic hosts include the  $\beta$ -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytichrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.



#### 4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

#### 5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

#### E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for

a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as  $^{32}\text{P}$  or  $^{35}\text{S}$ , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example,  $\text{CaPO}_4$ -mediated DNA transfection,

electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based

assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective

genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically

acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, PLURONICS™ or PEG.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon- (rhIFN- ), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *Bio/Technology*, 8:755-758 (1990); Cleland, "Design and Production of Single

Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

5 The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

10 This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

15 The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

20 In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

35 If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers

(Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for  $\beta$ -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are



prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

5 Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

10 These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

#### 15 F. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

##### 1. Polyclonal Antibodies

20 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate  
25 the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

##### 30 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an  
35 immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally,

either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal

antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

*In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

### 3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences

of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10, 779-783 (1992); Lonberg *et al.*, *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

#### 4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the

first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar  
10 size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been  
15 described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives  
20 is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized  
25 bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell  
30 culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by  
35 Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on

the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

#### 5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, *Anti-Cancer Drug Design*, 3: 219-230 (1989).

#### 7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

#### 8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).



### 9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

5 If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See,  
10 *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in  
15 amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques  
20 are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in  
25 the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and  $\gamma$  ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT<sup>TM</sup> (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.  
30 While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered  
35 to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

### G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

### EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

#### EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (*e.g.*, Dayhoff, GenBank), and proprietary databases (*e.g.* LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

5 Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

10 Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current  
15 Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized  
20 appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; *see*, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

#### EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

##### 25 1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linkered cDNA  
30 was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

##### 2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary  
35 cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

5 sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

### 3. Transformation and Detection

10 DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, *e.g.* CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

15 The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

20 The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL<sup>+</sup>, SUC<sup>+</sup>, GAL<sup>+</sup>. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (*e.g.*, SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

25 Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 30 2 x 10<sup>6</sup> cells/ml (approx. OD<sub>600</sub>=0.1) into fresh YEPD broth (500 ml) and regrown to 1 x 10<sup>7</sup> cells/ml (approx. OD<sub>600</sub>=0.4-0.5).

35 The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li<sub>2</sub>OOCCH<sub>3</sub>), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1  $\mu$ g, vol. < 10  $\mu$ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600  $\mu$ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li<sub>2</sub>OOCCH<sub>3</sub>, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500  $\mu$ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200  $\mu$ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

#### 4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30  $\mu$ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5  $\mu$ l) was used as a template for the PCR reaction in a 25  $\mu$ l volume containing: 0.5  $\mu$ l Klentaq (Clontech, Palo Alto, CA); 4.0  $\mu$ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5  $\mu$ l Kentaq buffer (Clontech); 0.25  $\mu$ l forward oligo 1; 0.25  $\mu$ l reverse oligo 2; 12.5  $\mu$ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:245)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:246)

PCR was then performed as follows:

- |    |    |              |                  |
|----|----|--------------|------------------|
| 35 | a. | Denature     | 92°C, 5 minutes  |
|    | b. | 3 cycles of: |                  |
|    |    | Denature     | 92°C, 30 seconds |
|    |    | Anneal       | 59°C, 30 seconds |

		Extend	72°C, 60 seconds
5	c.	3 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
	d.	25 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds
10	e.	Hold	4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5  $\mu$ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

#### EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

#### EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA94849-2960	PTA-2306	July 25, 2000
	DNA96883-2745	PTA-544	August 17, 1999
5	DNA96894-2675	PTA-260	June 22, 1999
	DNA100272-2969	PTA-2299	July 25, 2000
	DNA108696-2966	PTA-2315	August 1, 2000
	DNA117935-2801	PTA-1088	December 22, 1999
	DNA119474-2803	PTA-1097	December 22, 1999
10	DNA119498-2965	PTA-2298	July 25, 2000
	DNA119502-2789	PTA-1082	December 22, 1999
	DNA119516-2797	PTA-1083	December 22, 1999
	DNA119530-2968	PTA-2396	August 8, 2000
	DNA121772-2741	PTA-1030	December 7, 1999
15	DNA125148-2782	PTA-955	November 16, 1999
	DNA125150-2793	PTA-1085	December 22, 1999
	DNA125151-2784	PTA-1029	December 7, 1999
	DNA125181-2804	PTA-1096	December 22, 1999
	DNA125192-2794	PTA-1086	December 22, 1999
20	DNA125196-2792	PTA-1091	December 22, 1999
	DNA125200-2810	PTA-1186	January 11, 2000
	DNA125214-2814	PTA-1270	February 2, 2000
	DNA125219-2799	PTA-1084	December 22, 1999
	DNA128309-2825	PTA-1340	February 8, 2000
25	DNA129535-2796	PTA-1087	December 22, 1999
	DNA129549-2798	PTA-1099	December 22, 1999
	DNA129580-2863	PTA-1584	March 28, 2000
	DNA129794-2967	PTA-2305	July 25, 2000
	DNA131590-2962	PTA-2297	July 25, 2000
30	DNA135173-2811	PTA-1184	January 11, 2000
	DNA138039-2828	PTA-1343	February 8, 2000
	DNA139540-2807	PTA-1187	January 11, 2000
	DNA139602-2859	PTA-1588	March 28, 2000
	DNA139632-2880	PTA-1629	April 4, 2000
35	DNA139686-2823	PTA-1264	February 2, 2000
	DNA142392-2800	PTA-1092	December 22, 1999
	DNA143076-2787	PTA-1028	December 7, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA143294-2818	PTA-1182	January 11, 2000
	DNA143514-2817	PTA-1266	February 2, 2000
	DNA144841-2816	PTA-1188	January 11, 2000
5	DNA148380-2827	PTA-1181	January 11, 2000
	DNA149995-2871	PTA-1971	May 31, 2000
	DNA167678-2963	PTA-2302	July 25, 2000
	DNA168028-2956	PTA-2304	July 25, 2000
	DNA173894-2947	PTA-2108	June 20, 2000
10	DNA176775-2957	PTA-2303	July 25, 2000
	DNA177313-2982	PTA-2251	July 19, 2000
	DNA57700-1408	203583	January 12, 1999
	DNA62872-1509	203100	August 4, 1998
	DNA62876-1517	203095	August 4, 1998
15	DNA66660-1585	203279	September 22, 1998
	DNA34434-1139	209252	September 16, 1997
	DNA44804-1248	209527	December 10, 1997
	DNA52758-1399	209773	April 14, 1998
	DNA59849-1504	209986	June 16, 1998
20	DNA65410-1569	203231	September 15, 1998
	DNA71290-1630	203275	September 22, 1998
	DNA33100-1159	209377	October 16, 1997
	DNA64896-1539	203238	September 9, 1998
	DNA84920-2614	203966	April 27, 1999
25	DNA23330-1390	209775	April 14, 1998
	DNA32286-1191	209385	October 16, 1997
	DNA35673-1201	209418	October 28, 1997
	DNA43316-1237	209487	November 21, 1997
	DNA44184-1319	209704	March 26, 1998
30	DNA45419-1252	209616	February 5, 1998
	DNA48314-1320	209702	March 26, 1998
	DNA50921-1458	209859	May 12, 1998
	DNA53987	209858	May 12, 1998
	DNA56047-1456	209948	June 9, 1998
35	DNA56405-1357	209849	May 6, 1998
	DNA56531-1648	203286	September 29, 1998
	DNA56865-1491	203022	June 23, 1998



Table 7 (cont')

	DNA57694-1341	203017	June 23, 1998
	DNA57708-1411	203021	June 23, 1998
	DNA57836-1338	203025	June 23, 1998
	DNA57841-1522	203458	November 3, 1998
5	DNA58847-1383	209879	May 20, 1998
	DNA59212-1627	203245	September 9, 1998
	DNA59588-1571	203106	August 11, 1998
	DNA59622-1334	209984	June 16, 1998
	DNA59847-2510	203576	January 12, 1999
10	DNA60615-1483	209980	June 16, 1998
	DNA60621-1516	203091	August 4, 1998
	DNA62814-1521	203093	August 4, 1998
	DNA64883-1526	203253	September 9, 1998
	DNA64889-1541	203250	September 9, 1998
15	DNA64897-1628	203216	September 15, 1998
	DNA64903-1553	203223	September 15, 1998
	DNA64907-1163-1	203242	September 9, 1998
	DNA64950-1590	203224	September 15, 1998
	DNA64952-1568	203222	September 15, 1998
20	DNA65402-1540	203252	September 9, 1998
	DNA65405-1547	203476	November 17, 1998
	DNA66663-1598	203268	September 22, 1998
	DNA66667	203267	September 22, 1998
	DNA66675-1587	203282	September 22, 1998
25	DNA67300-1605	203163	August 25, 1998
	DNA68872-1620	203160	August 25, 1998
	DNA71269-1621	203284	September 22, 1998
	DNA73736-1657	203466	November 17, 1998
	DNA73739-1645	203270	September 22, 1998
30	DNA76400-2528	203573	January 12, 1999
	DNA76532-1702	203473	November 17, 1998
	DNA76541-1675	203409	October 27, 1998
	DNA79862-2522	203550	December 22, 1998
	DNA81754-2532	203542	December 15, 1998
35	DNA81761-2583	203862	March 23, 1999
	DNA83500-2506	203391	October 29, 1998
	DNA84210-2576	203818	March 2, 1999

Table 7 (cont')

	DNA86571-2551	203660	February 9, 1999
	DNA92218-2554	203834	March 9, 1999
	DNA92223-2567	203851	March 16, 1999
	DNA92265-2669	PTA-256	June 22, 1999
5	DNA92274-2617	203971	April 27, 1999
	DNA108760-2740	PTA-548	August 17, 1999
	DNA108792-2753	PTA-617	August 31, 1999
	DNA111750-2706	PTA-489	August 3, 1999
	DNA119514-2772	PTA-946	November 9, 1999
10	DNA125185-2806	PTA-1031	December 7, 1999

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

**EXAMPLE 5: Isolation of cDNA clones Encoding Human PRO6004, PRO5723, PRO3444, and PRO9940**

DNA molecules encoding the PRO840, PRO1338, PRO6004, PRO5723, PRO3444, and PRO9940 polypeptides shown in the accompanying figures were obtained through GenBank.

**EXAMPLE 6: Use of PRO as a hybridization probe**

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following

high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

#### EXAMPLE 7: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.71 g sodium citrate•2H<sub>2</sub>O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g

Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM  $\text{MgSO}_4$ ) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

*E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 8: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector.

Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

5 In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10  $\mu$ g pRK5-PRO DNA is mixed with about 1  $\mu$ g DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500  $\mu$ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M  $\text{CaCl}_2$ . To this mixture is added, dropwise, 500  $\mu$ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM  $\text{NaPO}_4$ , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is  
10 aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200  $\mu\text{Ci/ml}$   $^{35}\text{S}$ -cysteine and 200  $\mu\text{Ci/ml}$   $^{35}\text{S}$ -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15%  
15 SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Sompariyac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal  
20 density in a spinner flask and 700  $\mu$ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5  $\mu\text{g/ml}$  bovine insulin and 0.1  $\mu\text{g/ml}$  bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris.  
25 The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as  $\text{CaPO}_4$  or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as  $^{35}\text{S}$ -  
30 methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the  
35 pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells

can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by  $\text{Ni}^{2+}$ -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

- 5        Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

- 10        Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits  
15        selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect<sup>®</sup> (Qiagen), Dosper<sup>®</sup> or Fugene<sup>®</sup> (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately  $3 \times 10^7$  cells are frozen in an ampule for further growth and production as described below.

- 20        The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2  $\mu\text{m}$  filtered PS20 with 5% 0.2  $\mu\text{m}$  diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled  
25        with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with  $3 \times 10^5$  cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at  $1.2 \times 10^6$  cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is  
30        sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22  $\mu\text{m}$  filter. The filtrate was either stored at 4°C or immediately  
35        loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is

pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

5 Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275  $\mu$ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently  
10 desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 9: Expression of PRO in Yeast

15 The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal  
20 peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with  
25 Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 10: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG).  
35 A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding

the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni<sup>2+</sup>-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl<sub>2</sub>; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni<sup>2+</sup>-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A<sub>280</sub> with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A<sub>280</sub> baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni<sup>2+</sup>-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His<sub>10</sub>-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 11: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with



additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

#### EXAMPLE 12: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration

of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

#### EXAMPLE 13: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

#### EXAMPLE 14: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson,

Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins: In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

#### EXAMPLE 15: Pericyte c-Fos Induction (Assay 93)

This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100  $\mu$ l of PRO polypeptide test samples and controls (positive control = DME+5% serum +/- PDGF at 500 ng/ml; negative control = protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media = low glucose DMEM = 20% FBS + 1X pen strep + 1X fungizone. Assay Media = low glucose DMEM +5% FBS.

The following polypeptides tested positive in this assay: PRO982, PRO1160, PRO1187, and PRO1329.

**EXAMPLE 16: Chondrocyte Re-differentiation Assay (Assay 110)**

This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of the test PRO polypeptide, 5 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200 µl/well. After 5 days of incubation at 37°C, a picture of each well is taken and the differentiation state of the chondrocytes is determined. A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

The following polypeptide tested positive in this assay: PRO357.

**EXAMPLE 17: Identification of PRO Polypeptides That Stimulate TNF-α Release In Human Blood (Assay 128)**

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF-α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF-α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF-α release would be beneficial. Specifically, 200 µl of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300µl of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50µl of plasma is collected from each well and tested for the presence of TNF-α by ELISA assay. A positive in the assay is a higher amount of TNF-α in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay: PRO231, PRO357, PRO725, PRO1155, PRO1306, and PRO1419.

**EXAMPLE 18: Promotion of Chondrocyte Redifferentiation (Assay 129)**

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control)

or the test PRO polypeptide are added to give a final volume of 200  $\mu$ l/well. After 5 days at 37°C, 22  $\mu$ l of media containing 100 $\mu$ g/ml Hoechst 33342 and 50  $\mu$ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the > 50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

The following PRO polypeptides tested positive in this assay: PRO229, PRO1272, and PRO4405.

#### EXAMPLE 19: Normal Human Dermal Fibroblast Proliferation (Assay 141)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce proliferation of human dermal fibroblast cells in culture and, therefore, function as useful growth factors.

On day 0, human dermal fibroblast cells (from cell lines, maximum of 12-14 passages) were plated in 96-well plates at 1000 cells/well per 100 microliter and incubated overnight in complete media [fibroblast growth media (FGM, Clonetics), plus supplements: insulin, human epithelial growth factor (hEGF), gentamicin (GA-1000), and fetal bovine serum (FBS, Clonetics)]. On day 1, complete media was replaced by basal media [FGM plus 1% FBS] and addition of PRO polypeptides at 1%, 0.1% and 0.01%. On day 7, an assessment of cell proliferation was performed by Alamar Blue assay followed by Crystal Violet. Results are expressed as % of the cell growth observed with control buffer.

The following PRO polypeptides tested positive in this assay: PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO229, PRO1272, PRO181, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO788, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1194, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1488, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO5723, PRO1801, PRO4333, PRO3543, PRO3444, PRO4302, PRO4322, PRO5725, PRO4408, PRO9940, PRO7154, PRO7425, PRO6079, PRO9836 and PRO10096.

#### EXAMPLE 20: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes

overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from a panel of nine different tumor tissues (listed below) were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues, as compared to a non-cancerous human tissue control or other human tumor tissues. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

**TABLE 8**

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
PRO6004	colon tumor	universal normal control
PRO4981	colon tumor	universal normal control
PRO4981	lung tumor	universal normal control
PRO7174	colon tumor	universal normal control
PRO5778	lung tumor	universal normal control
PRO5778	breast tumor	universal normal control
PRO5778	liver tumor	universal normal control

TABLE 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
	PRO4332	colon tumor	universal normal control
5	PRO9799	colon tumor	universal normal control
	PRO9909	colon tumor	universal normal control
	PRO9917	colon tumor	universal normal control
10	PRO9917	lung tumor	universal normal control
	PRO9917	breast tumor	universal normal control
	PRO9771	colon tumor	universal normal control
15	PRO9877	colon tumor	universal normal control
	PRO9903	colon tumor	universal normal control
	PRO9830	colon tumor	universal normal control
20	PRO7155	colon tumor	universal normal control
	PRO7155	lung tumor	universal normal control
	PRO7155	prostate tumor	universal normal control
25	PRO9862	colon tumor	universal normal control
	PRO9882	colon tumor	universal normal control
	PRO9864	colon tumor	universal normal control
30	PRO10013	colon tumor	universal normal control
	PRO9885	colon tumor	universal normal control
35	PRO9879	colon tumor	universal normal control
	PRO10111	colon tumor	universal normal control
	PRO10111	rectal tumor	universal normal control
40	PRO9925	breast tumor	universal normal control
	PRO9925	rectal tumor	universal normal control
	PRO9925	colon tumor	universal normal control
	PRO9925	lung tumor	universal normal control
45	PRO9905	colon tumor	universal normal control
	PRO10276	colon tumor	universal normal control
	PRO9898	colon tumor	universal normal control
50	PRO9904	colon tumor	universal normal control
	PRO19632	colon tumor	universal normal control
55	PRO19672	colon tumor	universal normal control

TABLE 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
5	PRO9783	colon tumor	universal normal control
	PRO9783	lung tumor	universal normal control
	PRO9783	breast tumor	universal normal control
	PRO9783	prostate tumor	universal normal control
	PRO9783	rectal tumor	universal normal control
10	PRO10112	colon tumor	universal normal control
	PRO10284	colon tumor	universal normal control
	PRO10100	colon tumor	universal normal control
15	PRO19628	colon tumor	universal normal control
	PRO19684	colon tumor	universal normal control
	PRO10274	colon tumor	universal normal control
20	PRO9907	colon tumor	universal normal control
	PRO9873	colon tumor	universal normal control
	PRO10201	colon tumor	universal normal control
25	PRO10200	colon tumor	universal normal control
	PRO10196	colon tumor	universal normal control
	PRO10282	lung tumor	universal normal control
30	PRO10282	breast tumor	universal normal control
	PRO10282	colon tumor	universal normal control
	PRO10282	rectal tumor	universal normal control
	PRO10282	rectal tumor	universal normal control
35	PRO19650	colon tumor	universal normal control
	PRO21184	lung tumor	universal normal control
	PRO21184	breast tumor	universal normal control
	PRO21184	colon tumor	universal normal control
40	PRO21201	breast tumor	universal normal control
	PRO21201	colon tumor	universal normal control
45	PRO21175	breast tumor	universal normal control
	PRO21175	colon tumor	universal normal control
	PRO21175	lung tumor	universal normal control
50	PRO21340	colon tumor	universal normal control
	PRO21340	prostate tumor	universal normal control
	PRO21384	colon tumor	universal normal control
	PRO21384	lung tumor	universal normal control
	PRO21384	breast tumor	universal normal control



**EXAMPLE 21: Tissue Expression Distribution**

Oligonucleotide probes were constructed from the PRO polypeptide-encoding nucleotide sequence shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200-600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human adult and/or fetal tissue sources and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tissues tested. Knowledge of the expression pattern or the differential expression of the PRO polypeptide-encoding nucleic acid in various different human tissue types provides a diagnostic marker useful for tissue typing, with or without other tissue-specific markers, for determining the primary tissue source of a metastatic tumor, and the like. The results of these assays demonstrated the following:

(1) the DNA94849-2960 molecule is significantly expressed in the following tissues: cartilage, testis, colon tumor, heart, placenta, bone marrow, adrenal gland, prostate, spleen aortic endothelial cells and uterus, and not significantly expressed in the following tissues: HUVEC.

(2) the DNA100272-2969 molecule is significantly expressed in cartilage, testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, adrenal gland, prostate, spleen and aortic endothelial cells; and not significantly expressed in uterus. Among a panel of normal and tumor cells examined, the DNA100272-2969 was found to be expressed in normal esophagus, esophageal tumor, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

(3) the DNA108696-2966 molecule is highly expressed in prostate and also expressed in testis, bone marrow and spleen. The DNA108696-2966 molecule is expressed in normal stomach, but not expressed in stomach tumor. The DNA108696-2966 molecule is not expressed in normal kidney, kidney tumor, normal lung, or lung tumor. The DNA108696-2966 molecule is highly expressed in normal rectum, lower expression in rectal tumor. The DNA108696-2966 molecule is not expressed in normal liver or liver tumor. The DNA108696-2966 molecule is not expressed in normal esophagus, esophageal tumor, cartilage, HUVEC, colon tumor, heart, placenta, adrenal gland, aortic endothelial cells and uterus.

(4) the DNA119498-2965 molecule is significantly expressed in the following tissues: highly expressed in aortic endothelial cells, and also significantly expressed in cartilage, testis, HUVEC, colon tumor, heart, placenta, bone marrow, adrenal gland, prostate and spleen. It is not significantly expressed in uterus.

(5) the DNA119530-2968 molecule is expressed in the following tissues: normal esophagus and not expressed in the following tissues: esophageal tumors, stomach tumors, normal stomach, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumors, normal liver or liver tumors.

(6) the DNA129794-2967 molecule is significantly expressed in testis and adrenal gland; and not significantly expressed in cartilage, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, prostate, spleen, aortic endothelial cells and uterus.

(7) the DNA131590-2962 molecule is significantly expressed in the following tissues: bone marrow, adrenal

gland, prostate, spleen, uterus, cartilage, testis, colon tumor, heart, and placenta, and not significantly expressed in the following tissues: HUVEC, and aortic endothelial cells.

(8) the DNA149995-2871 molecule is highly expressed in testis, and adrenal gland; expressed in cartilage, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, prostate and uterus; weakly expressed in bone marrow, spleen and aortic endothelial cells; and not significantly expressed in placenta.

5 (9) the DNA167678-2963 molecule is significantly expressed in the following tissues: normal esophagus, esophageal tumor, highly expressed in normal stomach, stomach tumor, highly expressed in normal kidney, kidney tumor, expressed in lung, lung tumor, normal rectum, rectal tumor, weakly expressed in normal liver, and not significantly expressed in liver tumor.

10 (10) the DNA168028-2956 molecule is highly expressed in bone marrow; expressed in testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, adrenal gland, prostate, spleen, aortic endothelial cells and uterus; and is weakly expressed in cartilage. Among a panel of normal and tumor samples examined, the DNA168028-2956 was found to be expressed in stomach tumor, normal kidney, kidney tumor, lung tumor, normal rectum and rectal tumor; and not expressed in normal esophagus, esophageal tumor, normal stomach, normal lung, normal liver and liver tumor.

15 (11) the DNA176775-2957 molecule is highly expressed in testis; expressed in cartilage and prostate; weakly expressed in adrenal gland, spleen and uterus; and not significantly expressed in human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow and aortic endothelial cells.

20 (12) the DNA177313-2982 molecule is significantly expressed in prostate and aortic endothelial cells; and not significantly expressed in cartilage, testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, adrenal gland, spleen and uterus. Among a panel of normal and tumor cells, the DNA177313-2982 molecule was found to be expressed in esophageal tumor but not in normal esophagus, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16),  
5 Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54),  
10 Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92),  
15 Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), and Figure 244 (SEQ ID NO:244).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figures 1A-1B (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25),  
5 Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figures 59A-59B (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), and Figure 243 (SEQ ID NO:243).  
35

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence

selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figures 1A-1B (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figures 59A-59B (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), and Figure 243 (SEQ ID NO:243).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of Claim 1.
6. A host cell comprising the vector of Claim 5.
7. The host cell of Claim 6, wherein said cell is a CHO cell.
8. The host cell of Claim 6, wherein said cell is an *E. coli*.
9. The host cell of Claim 6, wherein said cell is a yeast cell.
10. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.
11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure

166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), and Figure 244 (SEQ ID NO:244).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:  
(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ

ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure



64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), with its associated signal peptide; or

(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ

ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide.

19. An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ

ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide;

(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ

ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure

138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide.

20. A method for stimulating the proliferation of or gene expression in pericyte cells, said method comprising contacting said cells with a PRO982, PRO1160, PRO1187, or PRO1329 polypeptide, wherein the proliferation of or gene expression in said cells is stimulated.

21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO357, PRO229, PRO1272 or PRO4405 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

22. A method for stimulating the release of TNF- $\alpha$  from human blood, said method comprising contacting said blood with a PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide, wherein the release of TNF- $\alpha$  from said blood is stimulated.

23. A method for stimulating the proliferation of normal human dermal fibroblast cells, said method comprising contacting said cells with a PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO229, PRO1272, PRO181, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO788, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1194, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1488, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO5723, PRO1801, PRO4333, PRO3543, PRO3444, PRO4302, PRO4322, PRO5725, PRO4408, PRO9940, PRO7154, PRO7425, PRO6079, PRO9836 or PRO10096 polypeptide, wherein the proliferation of said cells is stimulated.

24. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

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25. The method of Claim 24, wherein said tumor is lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, or liver tumor.

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26. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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**FIGURE 1A**

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTG  
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCCTCCTGCCTCCCGGTGGACAGA  
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTG  
CTTAGGTGTTATTTGGAAGATGGAGCTTCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTAT  
TTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA  
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTGTTCT  
GTTCAGACTCAACATACACCCAGAACAAATGCAGGTGCATCTAACTGTGCAAGTTCTCTCTAA  
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT  
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCCATCAGCAAAACCA  
TTTGAAGTGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA  
ATGCAGTGCAGGAAATGATGTGTGTCATCCCAGATGTGAGGAAAGTAAAGTTGTTGTCAACT  
TTGCTCCTACTATTTCAGGAAATTAATCTGGCACCGTGACCCCCGGACGCAGTGGCCTGATA  
AGATGTGAAGGTGCAGGTGTGCCGCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT  
CTTCAATGGCCAACAAGGAATTATTATTCAAATTTTAGCACAAGATCCATTCTCACTGTTA  
CCAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACA  
ACCAATGCGAGCCTGCCTCTTAACCCTCCAAGTACAGCCAGTATGGAATTACCGGGAGCGC  
TGATGTTCTTTTCTCCTGCTGGTACCTTGTGTTGACACTGTCTCTTTACCAGCATATTCT  
ACCTGAAGAATGCCATTCTACAATAAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCT  
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAGCAGCGTGGGATATAATC  
AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAAT  
TCTACTCTTTTTTTGATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCTTTTTTTAAG  
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAACTAC  
AACTTTTCAAAGCATTTCAGTCATGGTCTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAA  
TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTTCCCTGTTTCAAT  
AAGAGTCAATCCACATTTACAAAGATGCATTTTTTTTCTTTTTTGATAAAAAAGCAAATAA  
TTGCCCTCAGATTATTTCTTCAAATATAACACATATCTAGATTTTTCTGCTCGCATGATAT  
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTCTCTGT  
AAGTTCAGCATGGGTGTGCCTTCATACAATAATATTTTTCTCTTTGTCTCCAATAATATAA  
AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCAGAGTGATCAAGTTAAACCA  
TACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCTCTGCACTGACAA  
TGGGGTTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAAC  
AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA  
AATCATTCCCTTTAAATGACAGCACAGTCCACTCAAAGGATTGCCTAGCAATACAGCATCT  
TTTCTTTTCACTAGTCCAAGCCAAAAATTTTAAGATGATTTGTCAGAAAGGGCACAAAGTCC  
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTAATTTTATTTTGTGGCAGCTAA  
GTTAGTATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA  
GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAAATATATTA  
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAATAGCTAATTCTTCAATAA  
AATCTTTCTATATAGCCATTTTCAGTGCAAACAAGTAAATCAAAAAGACCATCCTTTATTT  
TTCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAATAT  
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAA  
AACTACATTTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG  
TTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTT  
ACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCCTTTTACAAGTTGTAACAACAAAG  
ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAG  
TATGTTGCCCTAGCAGGGATGGCTTAAAACTGTGATTTTTTTTCTTCAAGTAAAACCTTAGT  
CCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG  
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAAT  
AAATGTATGACATTATTTTGATTGATACATTAAAAAAGAGTTTTTAGAACAAATATGGCATT  
TAACCTTTATTTATTTTGTCTTTAAGAAATATCTTTGTGGAATTGTTGAATAAATAATAA  
AATATTATTTTGTATTGCAGCTTTAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

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**FIGURE 1B**

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC  
AAGAATGCATATTATTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT  
TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG  
ATTCCAAATTTGTGGAGTCTGGTGTTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT  
CAGTAGCTATATGTATTTGCCCTTTATGTTAGAAGAGACTTCTTGAGTGACATTTTTTAAATA  
GAGGAGGTATTCACTATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA  
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT  
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTTATGGACATATAA  
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTCAGAATAG  
CAGTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCATTTCAAG  
ANTATATTTTCTACAAGTTCCACTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTTAAAG  
AAGGAAGAAAGAAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAAGAAAAAGAATG  
AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG  
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGAAGGAAGAATCAGAGTATTAGG  
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA  
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAGTTCCTATTATGCAGCAATTATAT  
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGGAGACACTAAAAGATTTGAG  
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG  
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAAGTGAAGAAATTACCCAG  
GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA  
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG  
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA  
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA  
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA  
GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA  
CATCCATATTTATAACCTGATGTAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC  
TCAGTTTATCAATTAAAAAAA



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**FIGURE 2**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
><MW: 38719, pI: 6.12, NX(S/T): 6
MDMMLLVQGACCSNQWLA AVL LSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYL
EDGASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKR DYS LQIQNV DVTDDG PYTCSVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYECSAENDVSFPDVRKVKV VVNFAPT IQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASL
PLNPPSTAQYGITGSADVL FSCWYLV LTLSSFTSIFYLKNAILQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 322-343

**N-glycosylation sites.**

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

**Tyrosine kinase phosphorylation site.**

amino acids 180-188

**N-myristoylation sites.**amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,  
304-310, 321-327**Myelin P0 protein.**

amino acids 94-123

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**FIGURE 3**

CACTGCCCCGTCCGCTCTTCAGCAGCCGGTCGCGGGCGGTGGAAAAGCGAGTGAAGAGAGCGC  
GACGGCGGGCGGGCGGGCGGGCGGCAGCTATTGCTGGACGGCCAGTGGGAGAGCGAGGCCTGAG  
CCTCTGCGTCTAGGATCAAAATGTTTTCAATCCCAGAATACTATGAAGGCAAGAAGCTCCTC  
CTCACAGGAGCTACCGGTTTTCTAGGGAAGGTGCTTCTGGAAAAGTTGCTGAGGTCTTGTCC  
TAAGGTGAATTCAGTATATGTTTTGGTGAGGCAGAAAGCTGGACAGACACCACAAGAGCGAG  
TGGAAGAAGTCCTTAGTGGCAAGCTTTTTGACAGATTGAGAGATGAAAATCCAGATTTTAGA  
GAGAAAATTATAGCAATCAACAGCGAACTACCCAACTAACTGGCTCTCAGTGAAGAAGA  
TAAAGAGGTGATCATAGATTCTACCAATATTATATTCCACTGTGCAGCTACAGTAAGGTTTA  
ATGAAAATTTAAGAGATGCTGTTTCAAGTTAAATGTGATTGCAACGCGACAGCTTATTCTCCTT  
GCACAACAAATGAAGAATCTGGAAGTGTTTCATGCATGTATCAACAGCATATGCCTACTGTAA  
TCGCAAGCATATTGATGAAGTAGTCTATCCACCACCTGTGGATCCCAAGAAGCTGATTGATTCT  
TTAGAGTGGATGGATGATGGCCTAGTAAATGATATCACGCCAAAATTGATAGGAGACAGACC  
TAATACATACATATACACAAAAGCATTGGCAGAATATGTTGTACAACAAGAAGGAGCAAAAC  
TAAATGTGGCAATTGTAAGGCCATCGATTGTTGGTGCCAGTTGGAAAAGAACCTTTTCCAGGA  
TGGATTGATAACTTTAATGGACCAAGTGGTCTCTTTATTGCGGCAGGGAAAGGAATTCTTCG  
AACAAATACGTGCCTCCAACAATGCCCTTGCAAGTCTTGTTCCTGTAGATGTAGTTGTCAACA  
TGAGTCTTGCGGCAGCCTGGTATTCCGGAGTTAATAGACCAAGAAACATCATGGTGTATAAT  
TGTACAACAGGCAGCACTAATCCTTTCCACTGGGGTGAAGTTGAGTACCATGTAATTTCCAC  
TTTCAAGAGGAATCCTCTCGAACAGGCCTTCAGACGGCCCAATGTAAATCTAACCTCCAATC  
ATCTTTTATATCATTACTGGATTGCTGTAAGCCATAAGGCCCCAGCATTCTGTATGATATC  
TACCTCAGGATGACTGGAAGAAGCCCAAGGATGATGAAAACAATAACTCGTCTTCACAAAGC  
TATGGTGTCTTCTGAATATTTTCAAGTAATTCTTGGGTTTGGAAATACTGAGAATGTCAATA  
TGTTAATGAATCAACTAAACCCTGAAGATAAAAAGACCTTCAATATTGATGTACGGCAGTTA  
CATTGGGCAGAATATATAGAGAACTACTGCTTGGGAACTAAGAAGTACGTATTGAATGAAGA  
AATGTCTGGCCTCCCTGCAGCCAGAAAACATCTGAACAAGTTGCGGAATATACGTTATGGTT  
TTAATACTATCCTTGTGATCCTCATCTGGCGCATTTTTATTGCAAGATCACAAATGGCAAGA  
AATATCTGGTACTTTGTGGTTAGTCTGTGTTACAAGTTTTTGTGCATACTTCCGAGCATCCAG  
CACTATGAGATAC**TGA**AGACCAAGGATTGAGCATTAGAACATCTATACATATGGTGATCTAA  
ATGTACAAAATGTAAAATGTATAAGTCATCTCACTTTTTGTCAAGACATTAAACCATCTTAG  
ATCGGAGTGTGAAGTAAATTATGGTATATTTTATGTAAACATTTTAAATGTTTATGCTCATAAA  
ACTTAGTGAACACACTGTGTTATGCCAGCTCAAATCTACAGTAGCCACCAAAACCATGACTT  
AATATTTTGGGCCCTAGAAGAAAGGGGTGTGCTGAGGACAAGAGTGGGGAAATAGGAACACT  
GACCAGTATAACTGTGCAATTCTGGAACATATTAATTAAATAAATATGCCTTAACATATAGT  
GAATTTCTAATTCTAATGTTTCAAGTGAATGGAAGACATTTATTTGGACAGTATACTAGCAAA  
GTTGGTAGATATTTGATTCTTCATTTTTTTGTTTTTTTTCATTAGTTGAAGTGGGTTTTAGTTT  
TGTTTTAAAATTATAACCAGCGTATTTTTCACATCATCTGTAAAGTTAAATGATATCAAACATG  
AAAGAGATGTTCTCATTTTTCTTTTTCTGATTAAACGTCTGATGCATATCATTTTTCTATAA  
GTAATCAGTTGCTTTTAAATCAGAAGGCTATATTATTCTAATGACCCTATTTCGATCTAAAT  
GGGTTTGAAGATCCATATCAGCAACATACGTGTTTTTTGACAGAAAGTGAACAAATTCG  
TAAACTGTTAGTATCAAAAAGAAATAGGAATACAGTTTTCTTTTCCACATTATGATCAAATAA  
AATCTTGTGAGATTGTTAAAAA

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**FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA94849
><subunit 1 of 1, 515 aa, 1 stop
><MW: 59357, pI: 9.40, NX(S/T): 3
MVSIP EYYEGKNVLLTGATGFLGKVLLKLLRSCPKVNSVYVLVRQKAGQTPQERVEEVL
SGKLFDRRLRDENPDFREKIIA INSELTQPKLALSEEDKEVIIDSTNII FHCAATVRFNEN
LRDAVQLNVIATRQLILLAQQMKNLEVF MHVSTAYAYCNRKHIDEVYPPPPVDPKKLIDS
LEWMD DGLVNDITPKLIGDRPNTYIYTKALAEYVVQQEGAKLNVAIVRPSIVGASWKEPF
PGWIDNFNGPSGLFIAAGKGILRTIRASNNALADLVPVDVVVNMSLAAAWYSGVNRPRNI
MVYNCTTGSTNPFHWGEVEYHVISTFKRNP LEQAFRRPNVNLT SNHLLYHYWIAVSHKAP
AFLYDIYLRMTGRSPRMMKTITRLHKAMVFLEYFTS NSWVWNTENVNMLMNQLNPEDKKT
FNIDVRQLHWA EYIENYCLGTTKKYVLNEEMSGLPAARKHLNKL RNIRYGFNTILVILIWR
IFIARSQMARNIWIYFVVS L CYKFLSYFRASSTMRY
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 469-488

**N-glycosylation sites:**

Amino acids 283-287; 304-308; 341-345

**Tyrosine kinase phosphorylation site:**

Amino acids 160-169

**N-myristoylation sites:**

Amino acids 219-225; 252-258; 260-266; 452-458

**Leucine zipper pattern:**

Amino acids 439-461

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**FIGURE 5**

CGATGCCGGCGGTTCAGTGGTCCAGGTCCCTTATTCTGCCTTCTCCTCCTGCTCCTGGACCCC  
CACAGCCCTGAGACGGGGTGTCTCCTCTACGCAGGTTTGAGTACAAGCTCAGCTTCAAAGG  
CCCAAGGCTGGCATTGCCTGGGGCTGGAATACCTTCTGGAGCCATCATGGAGACGCCATCC  
TGGGCCTGGAGGAAGTGCGGCTGACGCCATCCATGAGGAACCGGAGTGGCGCCGTGTGGAGC  
AGGGCCTCTGTCCCCTTCTCTGCCTGGGAAGTAGAGGTGCAGATGAGGGTGACGGGACTGGG  
GCGCCGGGGAGCCCAGGGCATGGCCGTGTGGTACACCCGGGGCAGGGGCCATGTAGGCTCTG  
TCCTTGGGGGGCTGGCTTCGTGGGACGGCATCGGGATCTTCTTTGACTCTCCGGCAGAGGAT  
ACTCAGGACAGTCCTGCCATCCGTGTGCTGGCCAGCGACGGGCACATCCCCTCTGAGCAGCC  
TGGGGATGGAGCTAGCCAAGGGCTGGGCTCCTGTCAATTGGGACTTCCGGAACCGGCCACACT  
CCTTCAGAGCACGGATCACCTACTGGGGGCAGAGGCTGCGCATGTCTTGAACAGTGGCCTC  
ACTCCCAGTGATCCAGGTGAGTTCTGTGTGGATGTGGGGCCCCCTGCTTTTGGTCCCTGGAGG  
TTTCTTTGGGGTCTCAGCAGCCACCGGCACCCTGGCAGGTGAGGATCCCACTGGACAGGTTC  
CCCCTCAGCCCTTCTGGAGATGCAGCAGCTCCGCCTGGCGAGGCAGCTGGAAGGGCTGTGG  
GCAAGGCTGGGCTTGGGCACCAGGGAGGATGTAACCTCCAAAATCAGACTCTGAAGCTCAAGG  
AGAAGGGGAAAGGCTCTTTGACCTGGAGGAGACGCTGGGCAGACACCGCCGGATCCTGCAGG  
CTCTGCGGGGTCTCTCCAAGCAGCTGGCCCAGGCTGAGAGACAATGGAAGAAGCAGCTGGGG  
CCCCCAGGCCAAGCCAGGCCTGACGGAGGCTGGGGCCCTGGATGCTTCCTGCCAGATTCCATC  
CACCCCAGGGAGGGGTGGCCACCTCTCCATGTCACTCAATAAGGACTCTGCCAAGGTTCGGTG  
CCCTGCTCCATGGACAGTGGACTCTGCTCCAGGCCCTGCAAGAGATGAGGGATGCAGCTGTC  
CGCATGGCTGCAGAAGCCCAGGTCTCCTACCTGCCTGTGGGCATTGAGCATCATTTCTTAGA  
GCTGGACCACATCCTGGGCCTCCTGCAGGAGGAGCTTCGGGGCCCCGGCGAAGGCAGCAGCCA  
AGGCCCCCCGCCCCACCTGGCCAGCCCCCAAGGGCCTCCTCGTGCCTGCAGCCTGGCATCTTC  
CTGTTCTACCTCCTCATTCAGACTGTAGGCTTCTTCGGCTACGTGCACTTCAGGCAGGAGCT  
GAACAAGAGCCTTCAGGAGTGTCTGTCCACAGGCAGCCTTCCTCTGGGTCTGCACCACACA  
CCCCCAGGGCCCTGGGGATTCTGAGGAGGCAGCCTCTCCCTGCCAGCATGCCTGCCTGACCC  
ACCTCAGAGCCTGCTTTGCATCACTGGGAAGCAGGCAGTGTCTTGGGTGGGGGCTTGGTCAG  
TATCCTCTCCGTCTGGGTGCCCAGCTCCCACGCACACCTGAGCTTTCGGCATGCTCCACCT  
CGTTAAAGGTGATTTCCCTCTCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96883
><subunit 1 of 1, 514 aa, 1 stop
><MW: 55687, pI: 8.78, NX(S/T): 2
MPAVSGPGPLFCLLLLLLDPHSPETGCPPLRRFEYKLSFKGPRLALPGAGIPFWSHHGDA
ILGLEEVRLTPSMRNRSGAVWSRASVPFSAWEVEVQMRVTGLGRRGAQGMVWYTRGRGH
VGSVLGGLASWDGIGIFFDSPAEDTQDSPAIRVLASDGHIPSEQPGDGASQGLGSCHWDF
RNRPHSFRARITYWGQRLMSLNSGLTPSDPGEFCVDVGPLLLVPGGFFGVSAATGTLAG
EDPTGQVPPQPFLEMQQLRLARQLEGLWARLGLGTREDVTPKSDSEAQGEGERLFDLEET
LGRHRRILQALRGLSKQLAQAEQWKKQLGPPGQARPDGGWALDASCQIPSTPGRGGHLS
MSLNKDSAKVGALLHGQWTLLOALQEMRDAAVRMAAEQVSYLPVGIHHFLELDHILGL
LQEELRGPAKAAAKAPRPPGQPPRASSCLQPGIFLFYLLIQTVGFFGYVHFRQELNKSLO
ECLSTGSLPLGPAPHTPRALGILRRQPLPAMPA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 215-232;450-465

**N-glycosylation sites:**

Amino acids 75-79;476-480

**Glycosaminoglycan attachment site:**

Amino acids 5-9

**N-myristoylation sites:**Amino acids 78-84;122-128;126-132;168-174;172-178;  
205-211;226-232;230-236;236-242;356-362**Amidation site:**

Amino acids 102-106

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**FIGURE 7**

GGCCCCAGC**ATG**GCTTGGCAGGGCTGGCCCCGCGGCGTGGCAGTGGGTGCGCCGGCTGCTGGCT  
CCTCCTCGTCCTTGTCTCTGTCCTACTTGTGAGCCCCGCGGCTGCCGAGCGCGGCGGGGCC  
TCCGCGGTCTGCTCATGGCGCACAGCCAGCGGCTGCTCTTCCGAATCGGGTACAGCCTGTAC  
ACCCGCACCTGGCTCGGGTACCTCTTCTACCGACAGCAGCTGCGCAGGGCTCGGAATCGCTAC  
CCTAAAGGCCACTCGAAAACCCAGCCCCGCTCTTCAATGGAGTGAAGGTGCTTCCCATCCC  
TGTCTCTCGGACAACTACAGCTACCTCATCATCGACACCCAGGCCAGCTGGCTGTGGCTG  
TGGACCCCTCAGACCCCTCGGGCTGTGCAGGCTTCCATTGAAAAGGAAGGGGTACCTTGGTC  
GCCATTCTGTGTACTCACAAGCACTGGGACCACAGTGGAGGGAACCGTGACCTCAGCCGGCG  
GCACCGGGACTGTGCGGTGTACGGGAGCCCTCAGGACGGCATCCCCTACCTCACCCATCCCC  
TGTGTCATCAAGATGTGGTCAGCGTGGGACGGCTTCCAGATCCGGGCCCTGGCTACACCTGGC  
CACACACAAGGCCATCTGGTCTACCTACTGGATGGGGAGCCCTACAAGGGTCCCTCCTGCCT  
CTTCTCAGGGGACCTGCTCTTCTCTCTGGCTGTGGGCGGACCTTTGAGGGCAATGCAGAGA  
CCATGCTGAGCTCACTGGACACTGTGCTGGGGCTAGGGGATGACACCCCTTCTGTGGCCTGGT  
CATGAGTATGCAGAGGAGAACCTGGGCTTTGCAGGTGTGGTGGAGCCCGAGAACCTGGCCCG  
GGAGAGGAAGATGCAGTGGGTGCAGCGGCAGCGGCTGGAGCGCAAGGGCACGTGCCCATCTA  
CCCTGGGAGAGGAGCGCTCCTACAACCCGTTCTGAGAACCCTGCTGGCGCTACAGGAG  
GCTCTGGGGCCGGGGCCGGGCCCCACTGGGGATGATGACTACTCCCGGGCCAGCTCCTGGA  
AGAGCTCCGCGGGCTGAAGGATATGCACAAGAGCAAG**TGA**TGCCCCCAGCGCCCCCAGCCCA  
GCCCCTCCCCGCATGGGGAGGCCGCCACCACCAACACCTCATCATCCTTCTCATCGCTAAC  
ACCACCACCTCCATCGGCACCCAAAGCGGGCATCATCCCCCACAAGTCTCAGGGGAGGGGAG  
GGATCAGGCGATGAGACTGTGAGGCCAAAAGAAGGGGGCCTGTTGGAGGCTGGGAACCCCGC  
AGCGCGAGGCTGCCTCATCAACGGCAAGAGGAAAGGAGGGGTCTCGGGACATCTCCAGACCC  
TACCAACTGGGAGGGTCCCCCTCCTCCTTCCCTACTCCTGGGACGGCAGCAAGGACATGGGGG  
CTGCTGTTAGCTTCTCCGTGAGGAGGCTCATCTCACTGTAGCCCTGGAACCCAGGGTCCAT  
CTTGCCCTTCCCCCATCCATGGTTGGGAAAGAAGCTCAGCCCCCTCACAGTGGCCTCAAGTGT  
GATGCCTTACAAAAGCACCCTCAGATGGGCAGCTGGACTCTGGTGTCTGAGACTCTGCCC  
TCTTCCCACAGCCTCCCTGCCCCACCCATCCCTGCAAAGCCATTTTTCAGACAGAGCCATTC  
CTAAGAACACTGAAGGGCTGGAATGCTGGCTGGCCACTCTCTGCCTCAGTGGCCTCCCTACA  
GCCTGGAAGAAGGAGGGTCCCTGATTGCCAAGGAAACCTCCTCATTGGGCTAAGGAGACACTG  
GAGTCTGGAGTGTGGAGCCCCACAGTCTTGCAGGTACATGCTCTCCTTGACATCTGGCCT  
GGTTGTACCCACTGGCCTCTGCCTCTGCCCTGGGCCAAAAGGGCCCCCTCCTTGCCAGGGGAG  
AGACAGCCACGGTCTCTTTGGCCGATGCTGTATTCTCATTTTGGCCCTTGTCTTAGGCC  
GTCTGCCCCGCCCTCCTCCATCTAACCTTTCTGTTTTATCCGCAGCCCTTTTCTTCTTTGAG  
TTAGTAAAGATTTATTCTGTAACCTGACACTCATCTGGCCCTTTGCAGTTTGCCAGCCATATTC  
CCATGTGATTTCCCACTGGATCCAGGCCCCCATCCGGCTGGCAGGAGGGGGCTCTGACGTAC  
AGGTTGGAAATCAGAAGTCTGTGAGAGCGCGGGAGTGCATGGCAGCTCTGGGTCCCAGACCT  
GGCCCGACCCCTCTGCTTCACCTCCAGCTCTGCTGCTCCTCTACTCTTGGGTGAGATCCCT  
TTGGAGCCACAGCGAGGAACCCCTGTGGTCTCAGGCAGGTGTACCTTGAGTCAGCCAGGAGC  
CCTCTTTTCTGTGTCAAAGCCTGCCCTCGGGCTCTGCTCACCTCTGGTGACCTCCAAGAT  
GCCCCCTGCCCTCAGTTTCCCCCTCATGATCTGGCCTCTGCCCCCTTCTCTAGCCACAGCCTCT  
AGTACACTTTAGCAATACCACCAGACTAGTTAGAGTTCCCCACTCACCAAGCAAGACATGCA  
GTTTCATGCCTCTGTGCCTTCGCTCATGCTGTTTCTTCCGACTGGAATGCCTTCCCCTGCTC  
CTCCTGCCTTGTCTGCCTGGCAAGTTCATCTCTCAGATCCCCCTCAAAGGCCCCCTCCTCCA  
GGAAGGCAACCCCTGTGCCCTCCCCCTCCAGGCTACCTCTGCACTTTGTCAATGCTTCTCTT  
GTGGCACTTATCACACTGTATTTTACTTGTTTACATGTTTGTCTCCCCTTCTAGACTGTGAA  
TCCTTAAGGGCATGGACTGTATCTTATGCATCTCTGTATTTCTGCGCCTAGCACGGTGCCTA  
GCACACAGTAGGCGCTCAATAAATGTTGAATGAATGAAAAAAAAAAAAAAAAAAAAAAAAA  
AA  
AA

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**FIGURE 8**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96894
><subunit 1 of 1, 361 aa, 1 stop
><MW: 40747, pI: 9.20, NX(S/T): 1
MAWQGWPAAWQWVAGCWLLLVLVLLVSPRGCRARRGLRGLLMAHSQRLLFRIGYSLYT
RTWLGYLFIYRQQLRRARNRYPKGHSKTQPRLENGVKVLPPIVLSDNYSYLIIDTQAQLAV
AVDPSDPRAVQASIEKEGVTLVAILCTHKKHWDHSGGNRDLRRHRDCRVYGSPQDGI PYL
THPLCHQDVVSVGRLQIRALATPGHTQGHVLYLLDGEPIYKGPSCLFSGDLLFLSGCGRTF
EGNAETMLSSLDTVLGLGDDTLLWPGHEYAEENLGFAGVVEPENLARERKMQWVQRQRLE
RKGTCPSTLGEERSYNPFLRTHCLALQEALGPGPGPTGDDDISRAQLLEELRRLKDMHKS
K
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-35

**N-glycosylation site:**

Amino acids 106-110

**Glycosaminoglycan attachment site:**

Amino acids 234-238

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 301-305

**Tyrosine kinase phosphorylation site:**

Amino acids 162-171

**N-myristoylation sites:**

Amino acids 41-47;235-241;242-248;303-309

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 6-17

**cAMP phosphodiesterases class-II proteins:**

Amino acids 144-161

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**FIGURE 9**

GCTGACAATCCCCTTGACGTTCTATCCCGGAAGCTCCACCTGGGGCCCAATGTTGGGCGTGA  
TGTTCCCTCGCCTGTCTCTGCCTGGAAACTGGTCTTCCCAAGCTCCACTGGCAGCCACTTCT  
CCATGTTGGGCATCGGAGACATCGTTATGCCTGGTCTCCTACTATGCTTTGTCTTCGCTAT  
GACAACTACAAAAAGCAAGCCAGTGGGGACTCCTGTGGGGCCCCTGGACCTGCCAACATCTC  
CGGGCGCATGCAGAAGGTCTCCTACTCTCACTGCACCCTCATCGGATACTTTGTAGGCCTGC  
TCACTGCTACTGTGGCGTCTCGCATTCACCGGGCCGCCAGCCCGCCCTTCTCTATTTGGTG  
CCATTTACTTTATTGCCACTCCTCACGATGGCCTATTTAAAGGGCGACCTCCGGCGGATGTG  
GTCTGAGCCTTTCCACTCCAAGTCCAGCAGCTCCCGATTCTTGGAAAGTATGATGGATCACGT  
GGAAAGTGACCAGATGGCCGTCATAGTCCTTTTCTCTCAACTCATGGTTTGTTTCCTCTTAG  
AGCTGGCCTGGTACTCAGAAATGTACCTGTGTTTAAGGAACTGCCGTGTGACTGGATTTGGC  
ATTGAAAGGGAGCTCGTTTGCAGGAGAGAGGTGCTGGAGCCCTGTTTGGTTCCTTCTCTTCC  
TGCGGATGTAGAGGTGGGGCCCCTTCCAAGAGGGACAGGCCTCTCCCCAGCGCGCCTTCCTC  
CCACGTTTTTATGGATCTGCACCAGACTGTTACCTTCTGGGGGAGATGGAGATTTGACTGTT  
TAAAAACTGAAAACAGCGAGGAGTCTTTCTAGAACTTTTGAACACTAAAGGATGAAAAAT  
TAGC



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**FIGURE 10**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA100272
><subunit 1 of 1, 108 aa, 1 stop
><MW: 12055, pI: 4.69, NX(S/T): 0
MMDHVESDQMAVIVLFSQLMVCFLLELAWYSEMYLCLRNCRVTGFGIERELVCRREVLEP
CLVPSLPADVEVGPLPRGTGLSPARLPPTFLWICTRLLPSSGGDGLTV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**N-myristoylation site:**

Amino acids 80-86

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**FIGURE 11**

TCGCACACTGGTGGCTTCAGAAGAAATTCTCAACACCTAGCTCGCCAGAGAGTCTATGTATG  
GGATTGAACAATCTGTAACTAAAGGATCCTAATCATGAAAATAAGTATGATAAATTATAAG  
TCACTATTGGCACTGTTGTTTATATTAGCCTCCTGGATCATTTTTTACAGTTTTCCAGAACTC  
CACAAAGGTTTGGTCTGCTCTAACTTATCCATCTCCCTCCATTACTGGAACAACCTCCACAA  
AGTCCTTATTCCCTAAAACACCACTGATATCATTAAGCCACTAACAGAGACTGAACTCAGA  
ATAAAGGAAATCATAGAGAACTAGATCAGCAGATCCCACCCAGACCTTTCACCCACGTGAA  
CACCACCACCAGCGCCACACATAGCACAGCCACCATCCTCAACCCTCGAGATACGTACTGCA  
GGGGAGACCAGCTGCACATCCTGCTGGAGGTGAGGGACCCTTGGGACGCAGGAAGCAATAT  
GGCGGGGATTTCCCTGAGGGGCCAGGATGTCTTCCCCAGCGCTGATGGCAGGTGCTTCAGGAAA  
GGTGACTGACTTCAACAACGGCACCTACCTGGTCAGCTTCACTCTGTTCTGGGAGGGCCAGG  
TCTCTCTGTCTCTGCTGCTCATCCACCCCAAGTGAAGGGGTGTGAGCTCTCTGGAGTGCAAGG  
AACCAAGGCTATGACAGGGTGATCTTCACTGGCCAGTTTGTCAATGGCACTTCCCAAGTCCA  
CTCTGAATGTGGCCTGATCCTAAACACAAATGCTGAATTGTGCCAGTACCTGGACAACAGAG  
ACCAAGAAGGCTTCTACTGTGTGAGGCCTCAACACATGCCCTGTGCTGCACTCACTCACATG  
TATTCTAAGAACAAGAAAGTTTCTTATCTTAGCAAACAAGAAAAGAGCCTCTTTGAAAGGTC  
AAATGTGGGTGTAGAGATTATGGAAAAATTCAATACAATTAGTGTCTCCAAATGCAACAAAG  
AAACAGTTGCAATGAAAGAGAAATGCAAGTTTGGAAATGACATCCACAATCCCCAGTGGGCAT  
GTCTGGAGAAACACATGGAATCCTGTCTCCTGTAGTTTGGCTACAGTCAAAATGAAGGAATGC  
CTGAGAGGAAAACATATACCTAATGGGAGATTCCACGATCCGCCAGTGGATGGAATACTT  
CAAAGCCAGTATCAACACACTGAAGTCAGTGGATCTGCATGAATCTGGAAAATTGCAACACC  
AGCTTGCTGTGGATTTGGATAGGAACATCAACATCCAGTGGCAAAAATATTGTTATCCCTTG  
ATAGGATCAATGACCTATTCAGTCAAAGAGATGGAGTACCTCACCCGGGCCATTGACAGAAC  
TGGAGGAGAAAAAATACTGTCATTGTTATTTCCCTGGGCCAGCATTTTCAGACCCTTTCCCA  
TTGATGTTTTTATCCGAAGGGCCCTCAATGTCCACAAAGCCATTGAGCATCTTCTTCTGAGA  
AGCCCAGACACTATGGTTATCATCAAAACAGAAAACATCAGGGAGATGTACAATGATGCAGA  
AAGATTTAGTGACTTTTCATGGTTACATTCAATATCTCATCATAAAGGACATTTTCCAGGATC  
TCAGTGTGAGTATCATTGATGCCTGGGATATAACAATTGCATATGGCACAAATAATGTACAC  
CCACCTCAACATGTAGTCGGAAATCAGATTAATATATTATTAACTATATTTGTTAAATAACAA

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**FIGURE 12**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108696

&gt;&lt;subunit 1 of 1, 544 aa, 1 stop

&gt;&lt;MW: 62263, pI: 9.17, NX(S/T): 7

MKISMINYKSLALLFILASWIIFTVFQNSTKVWSALNLSISLHYWNNSTKSLFPKTPLI  
SLKPLTETELRIKEIIEKLDQQIPPRPFTHVNTTTSATHSTATILNPRDTCRGDQLHIL  
LEVVDHLGRRKQYGGDFLRARMSSPALMAGASGKVTDFFNNGTYLVSFTLFWEGQVSLSL  
LIHPSEGVSALWSARNQGYDRVIFTGQFVNGTSQVHSECGLIILNTNAELCQYLDNRDQEG  
FYCVRPQHMPCAALTHMYSKNKKVSYLSKQEKSLFERSNVGVEIMEKFNTISVSKCNKET  
VAMKEKCKFGMTSTIPSGHVWRNTWNPVSCSLATVKMKECLRGKLIYLMGDSTIRQWMEY  
FKASINTLKSVDLHESGKLQHQLAVDLDRNINIQWQKYCYPLIGSMTYSVKEMEYLTRA  
DRTGGEKNTVIVISLGQHFRRPFIDVFIRRALNVHKAIQHLLLRSPDTMVIKTENIREM  
YNDARFSDFHGYIQYLIKIDIFQDLSVSIIDAWDITIAYGTNNVHPPQHVVGNOINILL  
NYIC

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-glycosylation sites:**

Amino acids 29-33;38-42;47-51;48-52;92-96;160-164;210-214

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 262-266

**Tyrosine kinase phosphorylation site:**

Amino acids 236-243;486-494

**N-myristoylation sites:**

Amino acids 206-212;220-226;310-316;424-430;533-539

**Amidation site:**

Amino acids 127-131

**Cell attachment sequence:**

Amino acids 113-116

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**FIGURE 13**

GCAAAGAGAAGACTGAAAGACAAACCTGGGTGCAGCCAGAGAGGTCCAGATAGATGAGCTTG  
TGGCATCCATTCCCCAAGTTCAGCCTAGGGACTCCACGTACCCCAGCTGGGTCTCATTGTTC  
CAGAACTGCATTAGTTAAGATTACCCAGACTTGGATTTCAAAGGAATACTTTTCATTGTTCCG  
TCTGTAACACGAAGTAATTGGGGCCAGCTGGATGTCAGGATGCGTGTGGTTACCATTGTAAT  
CTTGCTCTGCTTTTGCAAAGCGGCTGAGCTGCGCAAAGCAAGCCCAGGCAGTGTGAGAAGCC  
GAGTGAATCATGGCCGGGCGGGTGGAGGCCGGAGAGGCTCCAACCCGGTCAAACGCTACGCA  
CCAGGCCTCCCGTGTGACGTGTACACATATCTCCATGAGAAATACTTAGATTGTCAAGAAAG  
AAAATTAGTTTATGTGCTGCCTGGTTGGCCTCAGGATTTGCTGCACATGCTGCTAGCAAGAA  
ACAAGATCCGCACATTGAAGAACAACATGTTTTCCAAGTTTAAAAAGCTGAAAAGCCTGGAT  
CTGCAGCAGAATGAGATCTCTAAAATTGAGAGTGAGGCGTTCTTTGGTTTAAACAAACTCAC  
CACCTCTTACTGCAGCACAACCAGATCAAAGTCTTGACGGAGGAAGTGTTTCATTTACACAC  
CTCTCTTGAGCTACCTGCGTCTTTATGACAACCCCTGGCACTGTACTTGTGAGATAGAAACG  
CTTATTTCAATGTTGCAGATTCCCAGGAACCGGAATTTGGGGAACCTACGCCAAGTGTAAG  
TCCACAAGAACAATAAAAAAATAAAAAACTGCGGCAGATAAAATCTGAACAGTTGTGTAATGAAG  
AAAAGGAACAATTGGACCCGAAACCCCAAGTGTCAGGGAGACCCCAAGTCATCAAGCCTGAG  
GTGGACTCAACTTTTTGCCACAATTATGTGTTTCCCATACAAACACTGGACTGCAAAAGGAA  
AGAGTTGAAAAAAGTGCCAAACAACATCCCTCCAGATATTGTTAAACTTGACTTGTCTATACA  
ATAAAATCAACCAACTTCGACCCAAGGAATTTGAAGATGTTTCATGAGCTGAAGAAATTAAAC  
CTCAGCAGCAATGGCATTGAATTCATCGATCCTGCCGCTTTTTTAGGGCTCACACATTTAGA  
AGAATTAGATTTATCAAACAACAGTCTGCAAACTTTGACTATGGCGTATTAGAAGACTTGT  
ATTTTTTTGAACTCTTGTGGCTCAGAGATAACCCTTGGAGATGTGACTACAACATTCCTAC  
CTCTACTACTGGTTAAAGCACCCTACAATGTCCATTTTAATGGCCTGGAATGCAAAACGCCT  
GAAGAATACAAAGGATGGTCTGTGGGAAAATATATTAGAAGTACTATGAAGAATGCCCAA  
AGACAAGTTACCAGCATATCCTGAGTCATTTGACCAAGACACAGAAGATGATGAATGGGAAA  
AAAAACATAGAGATCACACCGCAAAGAAGCAAAGCGTAATAATTACTATAGTAGGATTAAGGT  
AGAAATTGTTCTGATTGTAATTAGTTTTGTATTTTCTATACTGGTGTTAGAAAACATATGTT  
TACATTTGATTAACCTGTGTTGCCTATTTATGCAGGGTAATCCAGCTAAAGGAAGCTTTCTTT  
AATTATAAGTATTATTGTGACTATTATAGTAATCAAGAGAATGCTATCATCTGCTTGCCTG  
TCCATTTGTGGAACAGCATCTGGTGATATGCAATTCCACACTGGTAACCTGCAGCAGTTGGG  
TCCTAATGATGGCATTAGACTTTTCATAATGTCTGTATAAATGTTTTTACTGCTTTTAGAAA  
ATAAAGAAAAAAACTTGGTTCATGTTTAAAA

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**FIGURE 14**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA117935

&gt;&lt;subunit 1 of 1, 440 aa, 1 stop

&gt;&lt;MW: 51670, pI: 8.70, NX(S/T): 2

MRVVTIVILLCFCKAAELRKASPGSVRSRVNHGRAGGRRGSNPVKRYAPGLPCDVITYL  
HEKYLDQCERKLVYVLPQWPDLLHMLLARNKIRTLKNNMFSKFKKLKSLDLQONEISKI  
ESEAFFGLNKLTLLQHNQIKVLTEEVFIYTPLLSYLRLYDNPWHCTCEIETLISMLQI  
PRNRNLGNYAKCESPQEQKNKKLRQIKSEQLCNEEKEQLDPKPQVSGRPPVIKPEVDSTF  
CHNYVPFIQTLDCRKRKELKKVPNNIPDIVKLDLSYNKINQLRPKEFEDVHELKKLNLSS  
NGIEFIDPAAFLGLTHLEELDLSNNSLQNFYGVLEDLYFLKLLWLRDNPWRCDYNIHYL  
YYWLKHHYNVHFNGLECKTPPEYKGWSVGKYIRSYEECPKDKLPAYPESFDQDTEDEW  
EKKHRDHTAKKQSVIITIVG

**Important features of the protein:****Signal peptide:**

Amino acids 1-15

**N-glycosylation sites:**

Amino acids 297-301;324-328

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 19-23;39-43;430-434

**N-myristoylation sites:**

Amino acids 24-30;37-43

**Amidation site:**

Amino acids 37-41

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**FIGURE 15**

CGGGCAGCAGCGCGGGCCCCAGCAGCCTCGGCAGCCACAGCCGCTGCAGCCGGGGCAGCCTC  
CGCTGCTGTCGCCTCCTCTGATGCGCTTGCCCTCTCCCGGCCCCGGGACTCCGGGAGA**AATGT**  
GGGTCTAGGCATCGCGGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCTTTGCGCTGCAA  
ATCCAGTGCTACCAGTGTGAAGAATTCCAGCTGAACAACGACTGCTCCTCCCCGAGTTCAT  
TGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAGAAAGAAGTGATGGAGCAAAGTGCCG  
GGATCATGTACCGCAAGTCCTGTGCATCATCAGCGGCCTGTCTCATCGCCTCTGCCGGGTAC  
CAGTCCTTCTGCTCCCCAGGGAACTGAACTCAGTTTGCATCAGCTGCTGCAACACCCCTCT  
TTGTAAACGGGCCAAGGCCCAAGAAAAGGGGAAGTTCTGCCTCGGCCCTCAGGCCAGGGCTCC  
GCACCACCATCCTGTTCTCAAATTAGCCCTCTTCTCGGCACACTGCT**TGA**AGCTGAAGGAGA  
TGCCACCCCTCCTGCATTGTTCTTCCAGCCCTCGCCCCCAACCCCCACCTCCCTGAGTGA  
GTTTCTTCTGGGTGTCCTTTTATTCTGGGTAGGGAGCGGGAGTCCGTGTTCTCTTTTGTTCC  
TGTGCAAATAATGAAAGAGCTCGGTAAAGCATTCTGAATAAATTCAGCCTGACTGAATTTTC  
AGTATGTACTTGAAGGAAGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTAACCGGAGT  
CAAGGCCAGGCTGGCAGAGTCAGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTA  
AGCCTCCAGTGTCCATTCCATCCCTGATGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGA  
CGTTTTCTTAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTCGCTTGACATTCAAACCTT  
CATGCTCCTGAAAACCATTTCTCTGCAGCAGAATTGGCTGGTTTCGCGCCTGAGTTGGGCTCT  
AGTGACTCGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCCTCGCTCTGAAAAGTGCT  
TAAGAAAATCTTCTCAGTTCTCCTTGCAAGGACTGGCGCCGGGACGCGAAGAGCAACGGGC  
GCTGCACAAAGCGGGCGCTGTCGGTGGTGGAGTGCGCATGTACGCGCAGGCGCTTCTCGTGG  
TTGGCGTGCTGCAGCGACAGGCGGCAGCACAGCACCTGCACGAACACCCGCCGAAACTGCTG  
CGAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGA  
AGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTCGTGCTTGGGTTTGGCC  
GCAGCCATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAG  
CCCTGGGCAGACACGAGCAGGAGGGAGAGACAGAGA

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## FIGURE 16

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119474
><subunit 1 of 2, 141 aa, 1 stop
><MW: 15240, pI: 8.47, NX(S/T): 1
MWVLGIAATFCGLFLLPGFALQIQCYQCEEFQLNNDCSSPEFIVNCTVNVQDMCQKEVME
QSAGIMYRKSCASSAACLIASAGYQSFCS PGKLNSVCISCCNTPLCNGPRPKKRGSSASA
LRPGLRTTILFLKLALESAHC
```

### Important features of the protein:

#### Signal peptide:

Amino acids 1-22

#### N-glycosylation site:

Amino acids 45-49

#### cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 113-117

#### N-myristoylation sites:

Amino acids 5-11;115-121;124-130

#### Ly-6 / u-PAR domain proteins:

Amino acids 94-107

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**FIGURE 17**

CGCAAAGCCGCCCTCGGGGCGCTC**ATG**GCGGGACGCCTCCTGGGAAAGGCTTTAGCCGCGGT  
GTCTCTCTCTCTGGCCTTGGCCTCTGTGACTATCAGGTCCTCGCGCTGCCGCGGCATCCAGG  
CGTTCAGAAACTCGTTTTTCATCTTCTTGGTTTCATCTTAATACCAACGTCATGTCTGGTTCT  
AATGGTTCCAAAGAAAATTCTCACAATAAGGCTCGGACGTCTCCTTACCCAGGTTCAAAAGT  
TGAACGAAGCCAGGTTCTAATGAGAAAGTGGGCTGGCTTGTTGAGTGGCAAGACTATAAGC  
CTGTGGAATACACTGCAGTCTCTGTCTTGGCTGGACCCAGGTGGGCAGATCCTCAGATCAGT  
GAAAGTAATTTTTCTCCCAAGTTTAACGAAAAGGATGGGCATGTTGAGAGAAAGAGCAAGAA  
TGGCCTGTATGAGATTGAAAATGGAAGACCGAGAAATCCTGCAGGACGGACTGGACTGGTGG  
GCCGGGGGCTTTTGGGGCGATGGGGCCCCAAATCACGCTGCAGATCCCATTATAACCAGATGG  
AAAAGGGATAGCAGTGGAAATAAAATCATGCATCCTGTTTCTGGGAAGCATATCTTACAATT  
TGTTGCAATAAAAAGGAAAGACTGTGGAGAATGGGCAATCCCAGGGGGGATGGTGGATCCAGGA  
GAGAAGATTAGTGCCACACTGAAAAGAGAATTTGGTGAGGAAGCTCTCAACTCCTTACAGAA  
AACCAGTGCTGAGAAGAGAGAAATAGAGGAAAAGTTGCACAAACTCTTCAGCCAAGACCACC  
TAGTGATATATAAGGGATATGTTGATGATCCTCGAAACACTGATAATGCATGGATGGAGACA  
GAAGCTGTGAACTACCATGACGAAACAGGTGAGATAATGGATAATCTTATGCTAGAAGCTGG  
AGATGATGCTGGAAAAGTGAAATGGGTGGACATCAATGATAAACTGAAGCTTTATGCCAGTC  
ACTCTCAATTCATCAAACCTTGTGGCTGAGAAACGAGATGCACACTGGAGCGAGGACTCTGAA  
GCTGACTGCCATGCGTTG**TAG**CTGATGGTCTCCGTGTAAGCCAAAGGCCACAGAGGAGCAT  
ATACTGAAAAGAAGGCAGTATCACAGAATTTATACTATAAAAAGGGCAGGGTAGGCCACTTG  
GCCTATTTACTTTCAAACAATTTGCATTTAGAGTGTTTCGCATCAGAATAACATGAGTAAG  
ATGAACTGGAACACAAAATTTTCAGCTCTTTGGTCAAAGGAATATAAGTAATCATATTTTG  
TATGTATTCGATTTAAGCATGGCTTAAATTAATTTAAACAATAATGCTCTTTGAAGAATC  
ATAATCAGAATAAAGATAAATTCTTGATCAGCTATA



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**FIGURE 18**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119498
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39125, pI: 8.53, NX(S/T): 2
MAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAFRNSFSSSWFHLNNTNVMMSGSNNGSKEN
SHNKARTSPYPGSKVERSQVPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNF
SPKFNEKDGHVERKSKNGLYEIEENGRPRNPAGRTGLVGRGLLGRWGPNHAADPIITRWKR
DSSGNKIMHPVSGKHILQFVAIKRKDCGEWAI PGMVDPGEKISATLKREFGEEALNSLQ
KTSAEKREIEEKLHKLFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLML
EAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDHAWSEDSEADCHAL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**N-glycosylation site:**

Amino acids 55-59

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 179-183

**N-myristoylation sites:**

Amino acids 53-59;56-62

**mutT domain signature:**

Amino acids 215-235

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**FIGURE 19**

CGAGGGCTCCTGCTGGTACTGTGTTTCGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAG  
GCCATGCAGCCATGTTCCGGGAGCCCTAATTGCACAGAAGCCCC**ATG**GGGAGCTCCAGACTGG  
CAGCCCTGCTCCTGCCTCTCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGC  
TTTCGCCACCTGCCCCACTGGAACACCCGCTGTCCTCTGGCCTCCCACACGGATGACAGTTT  
CACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTGGTGGGCCCTCTTCTCCACAAAGCCTT  
GGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGCTGTCAGGTGGCTCA  
GGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAAGTCTTCCACATTCAA  
GTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTCACC  
TGTCTGAGAAGAGCCATCACATTTCCATCCCCTCCCCAGACATCTCCCACAAGGGACTTCGC  
TCTAAAAGGACCCAACTTCGGATCCAGAGACATGGGAAAGTCTTCCAGATTGGACTCACA  
AAGGCATGGAGGACCCGAGTTCTCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTCGGGTGA  
CCATATCTTCAGGCCCTGAGGTACGCGTGCCTTTTGTACCAGTGGGCACTGGAGTGTGAA  
GAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTGGGGGCCACACTGTAGAGCTGCC  
TTATGAATTCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAAGAGGACACTGTGA  
GGCGCAAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAAGTCA  
GTGCACTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCC  
ACTGAAGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATAACCCTTTGCAAAGACCTCC  
CGAATGCCACGGCTCGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCC  
CAGCTCTGCTTCAAGTTCTCTTTTGGAAACAGCAGCCATGTTGAATGCCCCCACCAGACTGG  
GTCTCTCACATCCTGGAATGTAAGCATGGATACCCAAGCCCAGCAGCTGATTCTTCACTTCT  
CCTCAAGAATGCATGCCACCTTCAGTGCTGCCTGGAGCCTCCCAGGCTTGGGGCAGGACACT  
TTGGTGCCCCCGTGTACACTGTACAGCCAGGCCCGGGGCTCAAGCCCAGTGTCACTAGACCT  
CATCATTCCCTTCTGAGGCCAGGGTGCTGTGTCTTGTGCTGCTGGTGTGGCGGTGAGATGTCCAGTTTG  
CCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCA  
CTGCTGGCCCTCCTCACCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTC  
AGGCCCGGGCCAGCGCGGCCAGTGCTCCTCCTGCACGCGGCGGACTCGGAGGCGCAGCGGC  
GCCTGGTGGGAGCGCTGGCTGAACTGCTACGGGCAGCGCTGGGCGGCGGGCGCGACGTGATC  
GTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGTGGGCCCGCTGCCGTGGCTCTGGGCGGC  
GCGGACGCGCGTAGCGCGGGAGCAGGGCACTGTGCTGCTGCTGTGGAGCGGCGCCGACCTTC  
GCCCCGTGAGCGGCCCGACCCCCGCGCCGCGCCCCTGCTCGCCCTGCTCCACGCTGCCCCG  
CGCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC  
GCTGCGCGCCCTGCCGCGCTACCGCCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGG  
ACGCGCGGCCCTTTCGAGAGGCCACCAGCTGGGGCGCCCTTGGGGCGCGGCAGCGCAGGCAG  
AGCCGCTAGAGCTGTGCAGCCGGCTTGAACGAGAGGCCCGCCGACTTGCAGACCTAGGT**TC**  
**AG**CAGAGCTCCACCGCAGTCCCGGGTGTCT

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**FIGURE 20**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119502
><subunit 1 of 1, 667 aa, 1 stop
><MW: 74810, pI: 9.55, NX(S/T): 3
MGSSRLAALLLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSFSGSSAYIPCRW
WALFSTKPWCVRVWHCSRCLCQHLLSGGSGLQRLGFHLLVQKSKKSSTFKFYRRHKMPAP
AQRKLLPRRHLSEKSHHISIPSPDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFS
FDLLPEARAIRVTISSGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVELPYEFLLP
CLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQHTQMVMALTLRCPLKLE
AALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKFSFGNSSHVECPHOTGSL
TSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDL
IIPFLRPGCCVLVWRSDVQFAWKHLLCPDVSYRHLGLLILALLLALLTLLGVVLALTCTRRP
QSGPGPARPVLLLHAADSEAQRRLVGALAE LLRAALGGGRDVIVDLWEGRHVARVGPLPW
LWAARTRVAREQGTVLLLWSGADLRPVSGPDPRAPLLALLHAAPRPLLLLAYFSRLCAK
GDIPPLRALPRYRLRLDLRLLRALDARPF AEATSWGRLGARQRRQSRLELC SRLEREA
ARLADLG
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 455-472

**N-glycosylation sites:**

Amino acids 318-322;347-351;364-368

**Glycosaminoglycan attachment site:**

Amino acids 482-486

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 104-108;645-649

**Tyrosine kinase phosphorylation site:**

Amino acids 322-329

**N-myristoylation sites:**

Amino acids 90-96;358-364;470-476

**Eukaryotic cobalamin-binding proteins:**

Amino acids 453-462

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**FIGURE 21**

CGGCTCGAGGCCCTTTGTGAGGGCTGTGAGCTGCGCCTGACGGTGGCACC**ATG**AGCAGCTCA  
GGTGGGGCGCCCGGGGCGTCCGCCAGCTCTGCGCCGCCCGCGCAGGAAGAGGGCATGACGTG  
GTGGTACCGCTGGCTGTGTGCGCTGTCTGGGGTGCTGGGGGCAGTCTCTTGCGCGATCTCTG  
GCCTCTTCAACTGCATCACCATCCACCCTCTGAACATCGCGGCCGGCGTGTGGATGATCATG  
AATGCCTTCATCTTGTTGCTGTGTGAGGCGCCCTTCTGCTGCCAGTTCATCGAGTTTGCAA  
CACAGTGGCGGAGAAGGTGGACCGGCTGCGCTCCTGGCAGAAGGCTGTCTTCTACTGCGGGA  
TGGCGGTTCGTTCCCATCGTCATCAGCCTGACCCTGACCACGCTGCTGGGCAACGCCATCGCC  
TTTGCTACGGGGGTGCTGTACGGA CTCTGCTCTGGGCAAAAAGGGCGATGCGATCTCCTA  
TGCCAGGATCCAGCAGCAGAGGCAGCAGGCGGATGAGGAGAAGCTCGCGGAGACCCTGGAGG  
GGGAGCTGT**TGA**AGGGCTGGGCGCCCCCTCCCTCCCTGTCCCCTCTTCTGGCTCTGTGTGGGTC  
CAAGTGAGGCCCTGGACTGTCCACGCTGAGGCACAGCCTGGAGAGGGGGCCTTTGCACGTGTCC  
CTACACCTGGAGTCCTCTGCTCCTTTCTCCAGACTGGCTTAAGCCAGGAGCCACTGGCTGCT  
GGTGTGAGGGTCTGGGCTGCTGGACTTGAGGCAGAGCCTGCAGCAGCTGTGTGGACACTACC  
CAGCCCTACTCCTCTGCTGGGTGGGTCTGCAGATCTCACACCACAGACAGGGCTGCCTGTGA  
CCTGCTGTGACCTGGGAGCAGCTTCCCCTGGAGATGCTGGTCCTGGCTTGAGGGGAGGGGCA  
AGTGGGACCCTGCCACCTGGGCACTGAGCAGAGGGACCTCCCCAGCTCTCTTAGCAGGTGG  
AGCCCCAGGGCCTGGGACAGCCTGCCGCTGCCAGCAACCTCCCACTGCTGCCTAGGGTGCAG  
CGCCCACTGTCAACCCTGCCTTCTGAAGAAGCCACAGGGCTCCTAAGGTGCACCCCGGTACC  
TGGAAGTGCAGCCTTGGCAGTGA CTGGACAGCTGGGTGGGGGATGCTCCCTGCTGGCCCTGG  
GAACCTTGAGACAGGCCACCTCAAGGCCCTCGGCTGCCCTCCTCCCTGGGCCTGCTGGGGC  
CCCTAGGTTCTACCCATCACCCCCCGCCCCCTGCTGGCCTTGGTGCTAAGGAAGTGGGGAGAG  
CAGGCTCTCCCTGGCACCAGGGGTGCCACCCCTCTCCCTGGTGTGGCCCCGTCAACATCAGC  
CACAGCCCAGCCCCATTAGTGGGTTAGTGGGTCTGACCTCAGCCCCACTCAGGTGCTCCTGC  
TGGCCTGCCCAAGCCCTGCCCTCAGGGAGCTTCTGCCTTTTAAGAAGTGGGCAGAGGCCACAGT  
CACCTCCCCACACAGAGCTGTCCCCACTGCCCTGGGTGCCAGGCTGTCCGGAGCCAGGCCTA  
CCCAGGGAGGATGCAGAGAGCTGGTGCCAGGATGTGCACCCCCATATTCCCTCTGCCCTGT  
GGCCTCAGCCCGCTGGCCTCTCTGACCGTGAGGCTGGCTCTCAGCCATCGGGCAGGTGCCTG  
GTCAGGCCTGGCTTAGCCCAGGTGGGGCTTGGCAGAAGCGGGCGGGTGTGGAAGATATTCCA  
TCTGGGGCCAACCCCAGGCTGGGCCTGCGCTGAGCTTCTGGAGCGCAGGTACTGGGTCTTGC  
TAAGTGAAGTGTTCCTCCAGGAACACCTCTCGGGCCCATCTGCGTCTGAGGCTGGGAGTGGCA  
TCTGAGGCCGGGAGTGGCATCTGAGGCCAGGAGTGGCAGGCTGGTGGGCTGGGCGTGGGGTT  
TTCTGGGGCCCTGCCAGTACTGCCCTGGGGACTTGGTGGGCTCCTGGGTGAGCAGCATCCCA  
CCCCTGGGAGTCTGGCCAGCTGAGCCCCAGGGTGGCAGGGGCATTATAGCCTGGTGGACATG  
TGCCTTCAGGGTTCCCTCCGGGGCCACCTTCCTCAGGCCAGTGCTGGGTTCAAAGGGCTGTGT  
GTGTGTGTGTTTGTGTGTGTATGTATATGTGTGTGGGTGCACACATCTGTCCCATGTATGCA  
GTGAGACCTGTCTACCTCCCAACAAGGAGCAAGGGCTCTGCCCGCCCTCTGCTCATTCCCTACC  
CAGGTAGTGGGACCCCGGGCCCCCTTCTGCCTGGCTTGCTTCTGCCCTTTCCAGAGGG  
GTCTCACTGACAGCCAGAGACAGCAGGAGAAGGGTTGGCTGTGGATCAAGGAAGGCTGCCCC  
TGTACCCTGTGGGGAAATGGTGGGTGCATGGCTGGATGCAGAGGTGGAAGGCCCTGGGCCAC  
AGGCGAGAGTGGGCGTGTACCTGTCCCAGGTTCCCAGCAAGTCTGCAGCTGTGCAGTCTTG  
GGTCCCTGACCCTGTGCGCCAGGGGGCGTGCTGTCCAGCAGGGGCCCTGCCTTGCAAGGAA  
CGTCTCTCCGGCGGCTGGGCGGCTCCTGCCTGGTCTGGGCTGTGTGTGGCGCCCTTTCCCTCC  
TTGTTTGTTCCTCTGTGTCTGTGTGCGTCTTAAGCAATAAAGCGTGGCCGTGGGAAAAAAA  
AA

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**FIGURE 22**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119516
><subunit 1 of 1, 172 aa, 1 stop
><MW: 18470, pI: 5.45, NX(S/T): 0
MSSSGGAPGASASSAPPAQEEGMTWWYRWLCRLSGVLGAVSCAISGLENCITIHPLNIAA
GVWMIMNAFILLCEAPFCCQFIEFANTVAEKVDRLRSWQKAVFYCGMAVVPVIVISLTLT
TLLGNAIAFATGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-42

**Transmembrane domains:**

Amino acids 64-77;109-128

**Tyrosine kinase phosphorylation site:**

Amino acids 142-150

**N-myristoylation sites:**

Amino acids 5-11;6-12;9-15;35-41;38-44;46-52;124-130;132-138

**Amidation site:**

Amino acids 140-144

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**FIGURE 23**

GTGAAACACCCATGGTTTTATGCTCTATTTCTCTTTTCCTCATCTTCTTCCACATCCTCTTT  
CTGAATGTATCAAACACTTTCCTTGAAGTGGGGCACCAGGAGGGCCACTCCAGTCTCCAATG  
CAGGGACTCAGGGGCAGGGATCTCTGAGAAAGTGGCCATCTCGTTATTAAAGCTCTGTCCTC  
TGCTTCCCTCTCACCTCAGAAGCAGCCCGTTTATTCAACAGAGCTCCAGGTTGCCAGCTAGG  
GGTTTTCGGGACCATAGACCAAGCAACCCCGAGAGACTGAGTACTGACCTGCAGTTGTTCCAG  
AAACTCTGCTGGGAATTAGGTTGTGACCTAGAAGTGAACTGACACTAACAGTGAGAAGGCAG  
GGTAAGAATGCAGTCTAGAGCGCAACCTTTCTCCACTAGACTTGTAAGTAATTTAAGTGAAT  
CCTGTCCCCCTGGGGTTCTATCCTGGCTGGCTCTGCTGGTGAACCTGACTGGCCAGCATAGG  
GCACTTGATGAGACCCTGGAATGCTGAGGCCAGTTGGGCAGCAAGCTTTCACCTCATCCTTC  
TGCCCATCTATCCAGCCATTCAAACATTCATTGCGCTGAAGACATTTATCAAGCTCCTGCAA  
TGGGTCAGGCATCTGCTAGGCACTGGGGACACAGAGCTCACAGTCTCCTGGAGGGGGTGAGA  
GATGACTGACAGGTGGTCTGTGGTGCAGTGTGACCTGGGAATGCACACAGTACTGTGGAAAC  
ACGGGAGAGGCATCTAGCACAACTGAGAGGGCCAGGGGAGGCTTCCTGGCAGGTTTCCCTT  
TAACCATCTTAAGGGAAAGAGGCACTAGGTAGGAAAATAAAGGGACAGTGGTGTCCCAGACA  
GAGGGCACTCTACATGGAA

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**FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119530
><subunit 1 of 1, 113 aa, 1 stop
><MW: 12799, pI: 7.53, NX(S/T): 1
MVLCSISLFLIFFHILFLNVSNYFLEVGHQEGHSSLQCRDSGAGISEKVAISLLKLCPLL
PSHLRSSPFIQQSSRLPARGFRDHRPSNPERLSTDQLFQKLCWELGCDLEVN
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**N-glycosylation site:**

Amino acids 19-23

**Glycosaminoglycan attachment site:**

Amino acids 41-45

**N-myristoylation site:**

Amino acids 42-48

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**FIGURE 25**

CGGGCTCCGCGCGGTCCCACCTCCCGGCTCCCTTCGCCTCCAGGATGCGCTGAGCCCTACAA  
CACCCCCAGCGGCCGCCGGCTCCCCACGAGGTGTGAATGACAGAGGTGGTGCCATCCAGCG  
CGCTCAGCGAGGTACGCCTGCGCCTCCTCTGCCACGATGACATAGACACTGTGAAGCACCTG  
TGTGGCGACTGGTTCCCCATCGAGTACCCAGACTCATGGTATCGTGATATCACATCCAACAA  
GAAGTTCTTTTCCCTTGCTGCAACCTACAGAGGTGCCATTGTGGGAATGATAGTAGCTGAAA  
TTAAGAACAGGACCAAATAACATAAAGAGGATGGAGATATTCTAGCAACCAACTTCTCTGTT  
GACACACAAGTCGCGTACATCCTAAGTCTGGGCGTCGTGAAAGAGTTCAGGAAGCACGGCAT  
AGGTTCCCTCTTACTTGAAAGTTTAAAGGATCACATATCAACCACCGCCCAGGACCACTGCA  
AAGCCATTTACCTGCATGTCCTCACCACCAACAACACAGCAATAAACTTCTATGAAAACAGA  
GACTTCAAGCAGCACCCTATCTCCCCTATTACTACTCCATTTCGAGGGGTCTCAAAGATGG  
CTTCACCTATGTCCTCTACATCAACGGCGGGCACCCTCCCTGGACGATTTTGGACTACATCC  
AGCACCTGGGCTCTGCACTAGCCAGCCTGAGCCCTGCTCCATTCCGCACAGAGTCTACCGC  
CAGGCCCACAGCCTGCTCTGCAGCTTCCTGCCATGGTCGGGCATCTCTTCCAAGAGTGGCAT  
CGAGTACAGCCGGACCATGTGATGTGCGCTGGGCAGCCGCCACCAGGCCCCACCCTTCAGCC  
GCCCCGAGAGCCCGCCTTCCTGTCCATCTGACCCCTTCTGTTTTCTGCAAGGAGCTGCCAGC  
CATCTAACTGGGCTCGTCGGCCTGCCCCAGCTGCAGGCCCCGGTGCTACACGGGCTCGGGAAC  
AGAACATCGTGGGCATGCGCAGAGCATGCCATCCGTGGCAGGCTCTTCAGCTCCCCCTCCCT  
GCTTCTGGAAACCTCTGCCTGCTGCCCTGGCCCTGCCCCCTGCGCATGCACCATCCCCAGG  
GCTGACCCAGTGTGGCTGCATTCACTGGGAGGGGCTGCCCTCACTGGGCTCTCCCACTCCG  
CTGCCTGTTCTTGCACTCCTTCCTGGAAAGCTGGAGGGGACTTTCTCCTGCAAGGGAGGAA  
CGCAAGTATTATGGACACACTTGACCGTAAAGGCACAGGAGCCTCGGAACAAGGGGGCGCAA  
TAAAGGGAATGGCCCGTCCCCTTCCAGAACCAGCCCCAAGAAGCCTGGGGGGTGAGGAGTGG  
CCCCACTCCTCCATGAGGGGCTGATGAGGGGTGGGCAGCCTGGGGGAGGCTTTCCCTCGCAA  
GCACAGAGCTCTGAGGCTCAGCCCCCTGGCACAGGCGGTACGCATCAGGACGGTTCCCTACT  
CCTCAGCACTTCCGTGCAGTTACCAGTGCCCTGGGAGGTACACTGCCCGTCGGACCTTGG  
CATGCTCCATTCACTGACCTGCTGAGGACAGGCATCGCCGAGACTCCTTGGGTCTCCCCG  
CCCTCCCTCATGCTGCCACAAGCTGCTGCTCCAAGGCCTGGCCACATGCAGACAGGAGGAAG  
CTGAGCTCGACATTAGGCCTCAAGGCTGCCATCTGTCTTGTAGGGCCTGGCCTTGTGGGCAG  
GGGGCAGTCTGTGCCTTGTGGGGCCCTCAGCCTCTGAGGGCAGAGATGCTGTGAGTGCCGCA  
GGTGCATCACATACTTCTAGCATCCTCTCCACCCTGCATTCCAAATGCTGCTTGTGCTGCCTGC  
CCTGCCCTCCGATGCAGGGGTGGGGTGGGGGGCGGAGTCCCGCCAGCATAGCTGCAGTGTC  
ACAAAGCCATGGCAGAGGGTCTAGCGGCGCCACCCTGCCCCAGCCTGAGGAGGAGGGAGAG  
GGAGGAACAACCCTGGGCAGACGGGGTCTCAGGGACCTGTGTCTTCCGCCTCCAGAGCTGC  
CCAGCCACGGGCTCTCAGGGTGTGGGGCAGCCCCAGGTCCCCTCTTGAACCTCAGCTGGGGC  
CAGGGGCCCTCAGAATGAAGGCAGGCACCAGGCAGGAGCAGCATCCCCCTCCTTGACGGTGC  
TGGCAGGAGGGCCGCGCCATGCTGACTGCTTGAACCTCTGCTGACCTGACAGTGTGGCGGG  
AGGGCCGCACCATGCTGACTGCCTGAATCTCTGCTGAGGCTGCCTGCCTGCCGGGCCAGCT  
CAGCGCCCTCTCCACTGCGAATCAGTGGCGATCATGTGATTTCTATTTCTGCCCCACAGGGT  
AAGGGACGAGTCTTCTGGAAGGCTCTGCCATGGACATTTGTCTCGGGCTCAGAGGCCCCAC  
CCTGCCCCACACCTGCCCTAATCACTGCAGTGTCCAGCCAGTGTTGAACAGATTGTAGCG  
TTCTGTCTCATTACGAGCAAATAAATAGACTTTCATTGGGAAAAAAAAAAAAA



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**FIGURE 26**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA121772

&gt;&lt;subunit 1 of 1, 242 aa, 1 stop

&gt;&lt;MW: 27465, pI: 7.72, NX(S/T): 3

MTEVVPSSALSEVSLRLLCHDDIDTVKHLCDWFPDIEYPDSWYRDITSNKKFFSLAATYR  
GAIVGMIVAEIKNRTKIHKEDGDILATNFSVDTQVAYILSLGVVKEFRKHGIGSLLLESL  
KDHISTTAQDHCKAIYLVLTNTNNTAINFYENRDFKQHHYLPYYSIRGVLKDGFTYVLY  
INGGHPPWTILDYIQHLGSALASLSPCSIPHRVYRQAHSLLCSFLPWSGISSKSGIEYSR  
TM

**N-glycosylation sites:**

Amino acids 73-77;88-92;143-147

**N-myristoylation sites:**

Amino acids 61-67;65-71;198-204;235-241

**Matrixins cysteine switch motif:**

Amino acids 18-31

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**FIGURE 27**

GTTGGGCAGCAGCCACCCGCTCACCTCCATCCCCAGGACTTAGAGGGACGCAGGGCGTTGGG  
AACAGAGGACACTCCAGGCGCTGACCCTGGGAGGCCAGGACCAGGGCCAAAGTCCCGTGGGC  
AAGAGGAGTCCTCAGAGGTCCTTCATTCAGCGGTTCCGGGAGGTCTGGGAAGCCCACGGCCT  
GGCTGGGGCAGGGTCAACGCCGCCAGGCCGCC**ATG**GTCTGTGCTGGCTGCTGCTTCTGGTG  
ATGGCTCTGCCCCCAGGCACGACGGGCGTCAAGGACTGCGTCTTCTGTGAGCTCACCGACTC  
CATGCAGTGTCTTGGTACCTACATGCACTGTGGCGATGACGAGGACTGCTTCACAGGCCACG  
GGGTCGCCCCGGGCACTGGTCCGGTCATCAACAAAGGCTGCCTGCGAGCCACCAGCTGCGGC  
CTTGAGGAACCCGTCAGCTACAGGGGCGTCACCTACAGCCTCACCACCAACTGCTGCACCGG  
CCGCCTGTGTAACAGAGCCCCGAGCAGCCAGACAGTGGGGGCCACCACCAGCCTGGCACTGG  
GGCTGGGTATGCTGCTTCCTCCACGTTTGCTG**TGA**CCAACAGGGAGGACAGGGCCTGGGACT  
GTTCTCCCAGATCCGCCACTCCCCATGTCCCCATGTCCTTCCCCCACTAAATGGCCAGAGAG  
GCCCTGGACAACCTCTTGCGGCCCTGGCTTCATCCCTTCTAAGGCTGTCCACCAGGAGCCCG  
GTGCTAGGGGAAGCATCCCCAGGCCTGACTGAGCGGCAGGGGAGCACGGCCCGTGGGTTTGA  
TTGTATTACTCTGTTCCACTGGTTCTAAGACGCAGAGCTTCTCACATCTCAATCAGGATGCT  
TCTCTCCATTGGTAGCACTTTAGAGTCCATGAAATATGGTAAAAAATATATATATATCATAA  
TAAATGACAGCTGATGTTTCATGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125148
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13004, pI: 5.70, NX(S/T): 0
MVLCLWLLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
INKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTSLALGLGMLLP
PRL
```

### **Important features of the protein:**

#### **Signal peptide:**

Amino acids 1-13

#### **N-myristoylation sites:**

Amino acids 19-25;52-58;64-70;81-87;106-112

#### **Ly-6 / u-PAR domain proteins:**

Amino acids 84-97

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FIGURE 29

GGCATTTTGAAGCCCAGTGTTGCCAGGGGGCATCTCCTTTGTGTTTATGAGAGACCTGCA  
TTCTCCCTGGCTCAGTTCTCTCAGGCTCTCCAGAGCTCAGGACCTCTGAGAAGAATGGAGCC  
CTCCTGGCTTCAGGAACCTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTCTGCATGTCTC  
TGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATGATCAGAGCCCTGCAC  
CTGTTTCCTGCACCCCTGCCCACTGGTTCATGGCCACAAGGAGTTTTACCCAGTAAAGGA  
GTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTTCCCTTGTTGGGTGGAC  
CCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAGATTCTCCTGAAAAGACAA  
GATCCCAAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGGGTGGTTCGAGGACTTGTGAC  
CCTGGATGGTTCATAATGGAAAAAGCACCGCCAGATTGTGAAACCTGGCTTCAACATCAGCA  
TTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTTTCGGATGATGCTGAACAAATGGGAG  
GAACACATTGCCCAAACTCACGTCTGGAGCTCTTTCAACATGTCTCCCTGATGACCCTGGA  
CAGCATCATGAAGTGTGCCTTCAGCCACCAGGGCAGCATCCAGTTGGACAGTACCCTGGACT  
CATACCTGAAAGCAGTGTTCAACCTTAGCAAAATCTCCAACCAGCGCATGAACAATTTTCTA  
CATCACAACGACCTGGTTTTCAAATTCAGCTCTCAAGGCCAAATCTTTTCTAAATTTAACCA  
AGAACTTCATCAGTTCACAGAGAAAGTAATCCAGGACCGGAAGGAGTCTCTTAAGGATAAGC  
TAAAACAAGATACTACTCAGAAAAGGCGCTGGGATTTTCTGGACATACTTTTGAGTGCCAAA  
AGCGAAAACACCAAAGATTTCTCTGAAGCAGATCTCCAGGCTGAAGTGAAAACGTTTCATGTT  
TGCAGGACATGACACCACATCCAGTGCTATCTCCTGGATCCTTTACTGCTTGGCAAAGTACC  
CTGAGCATCAGCAGAGATGCCGAGATGAAATCAGGGAACCTAGGGGATGGGTCTTCTATT  
ACCTGGGAACACCTGAGCCAGATGCCTTACACCACGATGTGCATCAAGGAATGCCTCCGCCT  
CTACGCACCGGTAGTAAACATATCCCGGTTACTCGACAAACCCATCACCTTTCCAGATGGAC  
GCTCCTTACCTGCAGGAATAACTGTGTTTATCAATATTTGGGCTCTTCACCACAACCCCTAT  
TTCTGGGAAGACCCTCAGGTCTTTAACCCTTGAGATTCTCCAGGGAAAATTCTGAAAAAAT  
ACATCCCTATGCCTTCATACCATTCTCAGCTGGATTAAGGAACTGCATTGGGCAGCATTTTG  
CCATAATTGAGTGTAAGTGGCAGTGGCATTAACTCTGCTCCGCTTCAAGCTGGCTCCAGAC  
CACTCAAGGCCTCCCCAGCCTGTTTCGTCAAGTTGTCCTCAAGTCCAAGAATGGAATCCATGT  
GTTTGCAAAAAAAGTTTGCTAATTTTAAGTCCTTTTCGTATAAGAATTAATGAGACAATTTTCCT  
ACCAAAGGAAGAACAAAAGGATAAATATAATACAAAATATATGTATATGGTTGTTTGACAAA  
TTATATAACTTAGGATACTTCTGACTGGTTTTGACATCCATTAACAGTAATTTTAATTTCTT  
TGCTGTATCTGGTGAAACCCACAAAAACACCTGAAAAAACTCAAGCTGACTTCCACTGCGAA  
GGGAAATTATTGGTTTGTGTAAGTGGTAGAGTGGCTTTCAAGCATAGTTTGATCAAAAC  
TCCACTCAGTATCTGCATTACTTTTATCTCTGCAATATCTGCATGATAGCTTTATTCTCAG  
TTATCTTTCCCATAATAAAAAATATCTGCCAAA

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**FIGURE 30**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125150
><subunit 1 of 1, 505 aa, 1 stop
><MW: 59086, pI: 9.50, NX(S/T): 3
MEPSWLQELMAHPFLLLLILLCMSLLLFQVIRLYQRRRWMI RALHLFPAPPAHWFYGHKEF
YPVKEFEVYHKLMEKYP CAVPLWVGPFMTFFSVHDPDYAKILLKRQDPKSAVSHKILESW
VGRGLVTLDGSKWKKHRQIVKPGFNISILKIFITMMSESVRMMLNKWEEHIAQNSRLELF
QHVSLMTLDSIMKCAFSSHQGSIQLDSTLDSYLKAVFNLSKISNORMNFLHHNDLVFKFS
SQGQIFSKFNQELHQFTEKVIQDRKESLKDCLKQD TTQKRRWDFLDILLSAKSENTKDFS
EADLQAEVKT FMFAGHDTTSSAISWILYCLAKYPEHQQRDEIRELLGDGSSITWEHLS
QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHPYFWED
PQVENPLRFSRENSEKIHPYAFIPFSAGLRNCIGQHFAIECKVAVALTLLRFKLAPDHS
RPPQPVRQVVLKSKNGIHVF AKKVC

```

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**Transmembrane domain:**

Amino acids 451-470

**N-glycosylation sites:**

Amino acids 145-149;217-221;381-385

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 264-268

**N-myristoylation sites:**

Amino acids 243-249;351-357;448-454;454-460

**Cytochrome P450 cysteine heme-iron ligand signature:**

Amino acids 445-455

**Cytochrome P450 cysteine heme-iron ligand proteins:**

Amino acids 442-473

**FAD-dependent glycerol-3-phosphate dehydrogenase proteins:**

Amino acids 124-141

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**FIGURE 31**

TCCGCTGTCGCCCAGTCCCGGCCGCTGGCGGGAACTGACCTGGAGCAAGCAGGACCTTCCCT  
CCCACCTCTCCCGCCTGGCCTCCGCGGGAGTCCCCTACGATCCCGCTCAGCAGTGGGGCACT  
CGCTGAGGACAGCGAGTCCTGGGAGTGAGCCCAAGGCCACCCCTGGCCAGCCCAGGAGAGAT  
AGCCAGGGCAGGCCCAGCAGCCCGAGGCCAGGCTCTGGCCACGGCGGTCTCCGACATGGGAGA  
GACATTGTCTGCTTTTTATCCTGTTAACCTGTCTTCGGTGGTTGTGCCACGACATTCCCCAG  
GGTTCAGGTGCCCCGGTGGCCGAGGGTCAGTCCAGTGGTAGAGCCTTGCTCTCCTAGGCTCAT  
CCTGCTGGCGGTCTCCTGCTTCTGCTGTGTGGTGTACAGCTGGTTGTGTCCGGTTCTGCT  
GCCTCCGGAAGCAGGCACAGGCCAGCCACATCTGCCACCAGCACGGCAGCCCTGCGACGTG  
GCAGTCATCCCTATGGACAGTGACAGCCCTGTACACAGCACTGTGACCTCCTACAGCTCCGT  
GCAGTACCCACTGGGCATGCGGTTGCCCCCTGCCCTTTGGGGAGCTGGACCTGGACTCCACGG  
CTCCTCCTGCCTACAGCCTGTACACCCCGGAGCCTCCACCCTCCTACGATGAAGCTGTCAAG  
ATGGCCAAGCCCAGAGAGGAAGGACCAGCACTCTCCAGAAACCCAGCCCTCTCCTTGGGGC  
CTCGGGCCTAGAGACCACTCCAGTGCCCCAGGAGTCGGGCCCCAATACTCAACTACCACCTT  
GTAGCCCTGGTGCCCCCTTGAAGGAGGTAGGAGAACGGACCAGAGCTTGGAGAACTAATGCTT  
GGAGCCAAGGGCCCCAGCCCACCCACCGTCCACACATTGCTGTGGCCCCAACCTCGGTGC  
CATGTTACACCGGCCCTGGCGTCACCCACTAGGCAGGCTGCTGCTTTCAGCCTCAGCCCCT  
GGCCCAGCCCCAGCAGGCCCTCAGCCTGGAAGAGGCCCTTGGGCCTAAGCCTCGGGTGGGA  
GCTCAGGGCCACCTGTGACGTCTGCATCTTCTTGGAGAGAGAATAAAGTTTGTATTTAAGTGGT

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**FIGURE 32**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125151
><subunit 1 of 1, 194 aa, 1 stop
><MW: 20882, pI: 6.44, NX(S/T): 0
MERHCLLFILLTCLRWLCHDIPOGSGARWPRVSPVVEPCSPRLILLAVLLLLLLCGVTAGC
VRFCCLRKQAQAQPHLPPARQPCDVAVIPMDSDSPVHSTVTSYSSVQYPLGMRLPLPFGE
LDLDSTAPPAYSPLYTPEPPPSYDEAVKMAKPREEGPALSQKPSPLL GASGLETTTPVPQES
GPNTQLPPCSPGAP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 39-58

**N-myristoylation site:**

Amino acids 55-61

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 50-61

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**FIGURE 33**

CCTTGCTTGGTGCTTGGCACACACAAATCCAGTGGGCTACACAGGTTTTCCAGAAGCCCCAC  
GAGGTGGTAATGGTGCTGCTGATTTCAGACCCTGGGGGCCCTCATGCCCTCGCTGCCCTCCTG  
CCTCAGCAACGGCGTGGAGAGGGCAGGGCCCGAGCAGGAGCTCACCAGGCTGCTGGAGTTCT  
ACGACGCCACCGCCCACTTCGCCAAGGGCTTGGAGATGGCACTGCTCCCCACCTACATGAA  
CACAACTCTGGTAAAAGTCACGGAGCTGGTGGATGCTGTGTATGATCCATACAAACCCTACCAG  
CTGAAGTATGGCGACATGGAAGAGAGCAACCTCCTCATCCAGATGAGTGCTGTGCCTCTGGA  
GCATGGGGAAGTGATTGACTGTGTGCAGGAGCTGAGCCACTCCGTGAACAAGCTGTTTGGTC  
TGGCGTCTGCAGCCGTTGACAGATGCGTCAGATTCACCAATGGCCTGGGGACCTGCGGCCTG  
TTGTGAGCCCTGAAATCCCTCTTTGCCAAGTATGTGTCTGATTTACCAGCACTCTCCAGTC  
CATACGAAAGAAGTGCAAACCTGGACCACATTCCCTCCCAACTCCCTCTTCCAGGAAGATTGGA  
CGGCTTTTTCAGAACTCCATTAGGATAATAGCCACCTGTGGAGAGCTTTTTCGGGCATTGTGGG  
GACTTCGAGCAGCAGCTAGCCAACAGGATTTTGTCCACAGCTGGGAAGTATCTATCTGATTC  
CTGCAGCCCCCGGAGCCTGGCTGGTTTTTCAGGAGAGCATCTTGACAGACAAGAAGAACTCTG  
CCAAGAACCCATGGCAAGAATATAATTACCTCCAGAAAGATAACCCTGCTGAATATGCCAGT  
TTAATGGAAATACTTTATACCCTTAAGGAAAAAGGGTCAAGCAACCACAACCTGCTGGCTGC  
ACCTCGAGCAGCGCTGACTCGGCTTAACCAGCAGGCCACCAGCTGGCTTTCGATTCCGTGT  
TCCTGCGCATCAAACAACAGCTGTTGCTTATTTTGAAGATGGACAGCTGGAATACGGCTGGC  
ATCGGAGAAACCCCTCACAGATGAACTGCCCGCCTTTAGTCTCACCCCTCTCGAGTACATCAG  
CAACATCGGGCAGTACATCATGTCCCTCCCCCTGAATCTTGAGCCATTTGTGACTCAGGAGG  
ACTCTGCCTTAGAGTTGGCATTGCACGCTGGAAAGCTGCCATTTCCCTCCTGAGCAGGGGGAT  
GAATTGCCCCGAGCTGGACAACATGGCTGACAACTGGCTGGGCTCGATCGCCAGAGCCACAAT  
GCAGACCTACTGTGATGCGATCCTACAGATCCCTGAGCTGAGCCCACACTCTGCCAAGCAGC  
TGGCCACTGACATCGACTATCTGATCAACGTGATGGATGCCCTGGGCCTGCAGCCGTCCCGC  
ACCCTCCAGCACATCGTGACGCTACTGAAGACCAGGCCTGAGGACTATAGACAGGTCAGCAA  
AGGCCTGCCCCGTGCGCTGGCCACCACCGTGGCCACCATGCGGAGTGTGAATTACTTACCCC  
ACCACACACCGGACCACCAAGAGAGCCAGGGCTGCTGTTTCGTGACTCACCAGCACAGATTT  
GCTCAGAACTCTGCCCAAGATTGGGCAGAAGTTACTTTAAAAAGACTTGGTTCAGCTGGTC  
ACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGCCAGATGGATCATGAGGCC  
AGGAGTTCGAGACCAGCCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAAT  
TAACAGCAGAGCGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAGACTTGGTTCATTTGTATAA  
TCAAAAAGAGTTGTAAATTAAAGATGTATTATTTATCAGAGAAGACTTTTTAGATAATTTTT  
TTAAAGGATCAGATCTTGAAAATGGAATAAATACTACTGTGAAATGCAAAAA



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**FIGURE 34**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125181
><subunit 1 of 1, 491 aa, 1 stop
><MW: 54759, pI: 5.61, NX(S/T): 0
MVLLIQTLGALMPSLPSCLSNGVERAGPEQELTRLLEFYDATAHFAKGLEMALLPHLHEH
NLVKVTELVDVYDPYKPYQLKYGDMEESNLLIQMSAVPLEHGEVIDCVQELSHSVNKL
GLASAAVDRCVRFTNGLGTCGLLSALKSLFAKYVSDFTSTLQSIRKKCKLDHIPPNSLFQ
EDWTAFQNSIRIIATCGELLRHCGDFEQQLANRILSTAGKYLSDESCSPRSLAGFQESILT
DKKNSAKNPWQEYNYLQKDNPAEYASLMEILYTLKEKGSSNHNLLAAPRAALTRLNQOAH
QLAFDSVFLRIKQQLLLISKMDSWNTAGIGETLTDELPAFSLTPLEYISNIGQYIMSLPL
NLEPFVTQEDSALELALHAGKLPFPPEQGDELPELDNMADNWLGSIARATMQTYCDAILQ
IPELSPHSAKQLATDIDYLINVMDALGLQPSRTLQHIIVTLLKTRPEDYRQVSKGLPRRLA
TTVATMRSVNY
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 242-246

**N-myristoylation sites:**Amino acids 22-28; 48-54; 121-127; 136-142; 141-147; 328-334;  
447-453**Leucine zipper pattern:**

Amino acids 295-317

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**FIGURE 35**

GCAAGTGCCACCATGCTAGTGTGATTTGGACTTCAGTAAAAGTTAGTTTGCTTCCTTCCCGT  
TGTCCTCATCTCACTCCTGGGCCACCC**AT**GGGGCTGCTGGTAGCTGGTGTGTGGCTGCTGCTG  
GACTGTGTGGCAGTCCATCCATCTGTGTCAGCAGCCACTGCGGGCCTACTTGCTGGGTGCCAG  
CACCGCACTCACCCTGCAGGCGTGGCCAGGAGCGTGAGATCCCCAGAGCCCATGGCCAGTG  
AGAGGCGGCCAGGGATAGGTACCCAGGGAATGCCACAGGAGTTTGCTGGGCTCACGGAGCTC  
TTTCACTGGTCAGAGAGGAGTGTGTGTAGGAGAGGACTTCTACTTGGTGTTGAAGGACAGAT  
GGGGTTTGGCTGGGAGAGAGGAGGAATGTGGGCGGGCCTTATAGGCAGGCGAGAAGGTGAGA  
GCCAAGGCCCTCTGTGGGCAGGGCGAGGTGGCGTGTTGAGGAGACTCGTCCAGCTGGGCAGA  
GGCTCATGT**TC**AGGGGATGAGGCAGAGCTGGGGGAGGAGGGAGCCAGAAATGGCAGGTCCTT  
GAATGCAGGTTTGGGAAGCAGGGACGCCCTGTGAGGGTACAGAGTCTGGGCTGTTACCTTCTG  
TGGCTTTTGTAGAAAGGTGAGATGTCAGGGAGGAAGACAGGACTCCAGGATGTCTCCTGTCTCT  
CTCTGGAAAAAGGAGGTGGGCCCCCTTTCTCAGCAGTCAGCTGCTGTTTTTGGAGTCTTCTCC  
ATGGATAATCCACGGTGTGGGAAGTGGTTAAGGTAATGGATCCTCATGGGCTTACCATAAAA  
ATATCTGGAGGCTGGACCATTTTCTTAAACGTTATAAAAGCTGGAATTGAATGCCATCGG  
TGTCACCCCTGGGAAGTGTGCTTTCTCTTGAGCTCTTTTGGCCCCGAGATAGCAGTCACTCC  
ATAGTTTCGTGAAGACCAGCCTGGTGTGCTGCTGTTTCTGCCATTAGGGAGCAGCTAGAGG  
TCTTCCAGTAGCTCCTGTGTAAAGTGATGAAAGAAAAGGGCTGGGTGCTGACTGCTCCTGGA  
GAAAAGCAACACACTCCCAAAGTCTTAATTGCCTGCTTCCAGGGAGCTGTGGTGGTTTCCCT  
TGGGCAGGGCACACGCCCCAGTGGTTGACTTAATAAGGATACATTTTAATCAGAGGACAAAA  
ATGTGCCCTGACTTGATTTCCGCATGGGCTTCCAGCATGGTCAAAGG

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**FIGURE 36**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125192  
><subunit 1 of 1, 139 aa, 1 stop  
><MW: 14841, pI: 9.20; NX(S/T): 0  
MGLLVAGVWLLLDCAVHPSVSSHCGPTCWVPSTALT TAGVARSVRSPEPMASERRPGIG  
TQGMPQEFAGLTELFHWSERSVCRRGLLLGVEGQMFGWERRGGMWAGLIGRREGESQGPI  
WAGRGGVLRRLVQLGRGSC

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-myristoylation sites:**

Amino acids 2-8;40-46;86-92;102-108;103-109

**Amidation site:**

Amino acids 109-113

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**FIGURE 37**

GGCCAGGAATGGGGTCCCCGGGCATGGTGCTGGGCCTCCTGGTGCAGATCTGGGCCCTGCAA  
GAAGCCTCAAGCCTGAGCGTGCAGCAGGGGCCCAACTTGCTGCAGGTGAGGCAGGGCAGTCA  
GGCGACCCTGGTCTGCCAGGTGGACCAGGCCACAGCCTGGGAACGGCTCCGTGTAAAGTGGACA  
AAGGATGGGGCCATCCTGTGTCAACCGTACATCACCAACGGCAGCCTCAGCCTGGGGGTCTG  
CGGGCCCCAGGGACGGCTCTCCTGGCAGGCACCCAGCCATCTCACCCCTGCAGCTGGACCCTG  
TGAGCCTCAACCACAGCGGGGCGTACGTGTGCTGGGCGGCCGTAGAGATTCTGAGTTGGAG  
GAGGCTGAGGGCAACATAACAAGGCTCTTTGTGGACCCAGATGACCCACACAGAACAGAAA  
CCGGATCGCAAGCTTCCCAGGATTCTCTTCGTGCTGCTGGGGGTGGGAAGCATGGGTGTGG  
CTGCGATCGTGTGGGGTGCCTGGTTCTGGGGCCGCCGCAGCTGCCAGCAAAGGGACTCAGGA  
AATGCATTCTACAGCAACGTCCTATAACGGCCCCGGGGGGCCCCAAAGAAGAGTGAGGACTG  
CTCTGGAGAGGGGAAGGACCAGAGGGGCCAGAGCATTTATTCAACCTCCTTCCCGCAACCGG  
CCCCCGCCAGCCGCACCTGGCGTCAAGACCCTGCCCCAGCCCGAGACCCTGCCCCAGCCCC  
AGGCCCCGGCCACCCCGTCTCTATGGTCAGGGTCTCTCCTAGACCAAGCCCCACCCAGCAGCC  
GAGGCCAAAAGGGTTCCCCAAAGTGGGAGAGGAGTGAGAGATCCCAGGAGACCTCAACAGGA  
CCCCACCCATAGGTACACACAAAAAAGGGGGGATCGAGGCCAGACACGGTGGCTCACGCCTG  
TAATCCCAGCAGTTTGGGAAGCCGAGGCGGGTGGAAACACTTGAGGTCAGGGGTTTGAGACCA  
GCCTGGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAG  
CCTGGGCGACAGAGTGAGACTCCGTCTCAAAAAAAAAAACAAGCAGGAGGATTGGGAGCC  
TGTCAGCCCCATCCTGAGACCCCGTCCTCATTTCTGTAATGATGGATCTCGCTCCCACTTTC  
CCCCAAGAACCTAATAAAGGCTTGTGAAGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125196
><subunit 1 of 1, 278 aa, 1 stop
><MW: 30319, pI: 9.21, NX(S/T): 3
MGSPGMVLGLLVQIWALQEASSLSVQQGPNLLQVRQGSQATLVCQVDQATAWERLRVKWT
KDGAILCQPYITNGSLSLGVCGPQGRLSWQAPSHLTLQLDPVSLNHSGAYVCWAAVEIPE
LEEAEGNITRLFVDPDDPTQNRNRIASFPGFLFVLLGVGSMGVAAIVWGAWFWGRRSCQQ
RDSGNAFYNSVLYRPRGAPKKSEDCSGEGKDQRGQSIYSTSFPQPAPRQPHLASRPCPSP
RPCPSRPGRHPVSMVRVSPRPSPTQQPRPKGF PKVGEE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**Transmembrane domain:**

Amino acids 149-166

**N-glycosylation sites:**

Amino acids 73-77;105-109;127-131

**Glycosaminoglycan attachment site:**

Amino acids 206-210

**N-myristoylation sites:**

Amino acids 5-11;37-43;63-69;108-114

**Amidation site:**

Amino acids 173-179

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**FIGURE 39**

ACCAGCAGAAGGCTGGGAGTCTGTAGTTTGTTCCTGCTGCCAGGCTCCACTGAGGGGAACGG  
GGACCTGTCTGAAGAGAAGATGCCCCCTGCTGACACTCTACCTGCTCCTCTTCTGGCTCTCAG  
GCTACTCCATTGCCACTCAAATCACCGGTCCAACAACAGTGAATGGCTTGGAGCGGGGCTCC  
TTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGGTGTGAGG  
AGCTATTTGGCGTGAAGTCAAGATCCTTGTTAAAACCAGTGGGTCAGAGCAGGAGGTGAAGA  
GGGACCGGGTGTCCATCAAGGACAATCAGAAAAACCGCACGTTCACTGTGACCATGGAGGAT  
CTCATGAAAACCTGATGCTGACACTTACTGGTGTGGAATTGAGAAAACCTGGAAATGACCTTGG  
GGTCACAGTTCAAGTGACCATTGACCCAGCACAGTCAACCAAGAAGAACTAGCAGCTCCC  
CAACTCTGACCGGCCACCACTTGGACAACAGGCACAAGCTCCTGAAGCTCAGTGTCTCCTG  
CCCCTCATCTTCACCATATTGCTGCTGCTTTTGGTGGCCGCCTCACTCTTGGCTTGGAGGATG  
ATGAAGTACCAGCAGAAAGCAGCCGGGATGTCCCCAGAGCAGGTACTGCAGCCCCCTGGAGGG  
CGACCTCTGCTATGCAGACCTGACCTGCAGCTGGCCGGAACCTCCCCGCGAAAGGCTACCA  
CGAAGCTTTCCTCTGCCCAGGTTGACCAGGTGGAAGTGGAAATATGTCACCATGGCTTCCTTG  
CCGAAGGAGGACATTTCTATGCATCTCTGACCTTGGGTGCTGAGGATCAGGAACCGACCTA  
CTGCAACATGGGCCACCTCAGTAGCCACCTCCCCGGCAGGGGGCCCTGAGGAGCCCACGGAAT  
ACAGCACCATCAGCAGGCCTTAGCCTGCACTCCAGGCTCCTTCTTGGACCCCAGGCTGTGAG  
CACACTCCTGCCTCATCGACCGTCTGCCCCCTGCTCCCCCTCATCAGGACCAACCCGGGGACT  
GGTGCCTCTGCCTGATCAGCCAGCATTGCCCCCTAGCTCTGGGTGGGCTTGGGGCCAAGTCT  
CAGGGGGCTTCTAGGAGTTGGGGTTTTCTAAACGTCCCCCTCCTCTCCTACATAGTTGAGGAG  
GGGGCTAGGGATATGCTCTGGGGCTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGT  
TATCATTATTATCATGAAGTACCATTATCATAATAACAATGAACCTTTATTTATTGCCTACCA  
CATGTTATGGGCTGAATAATGGCCCCCAAAGATATCTGTGTCCTAATCCTCAGAACTTGTGA  
CTGTTACCTTCTGTGGCAGAAAGGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAGATA  
GAGAGGTATTCTTGCTGATTCAAGTGGGCCCAAATATCACCACAAGGGTCCTCATAAGAA  
AGAGGCCAGAAGGTCAAAGAGGTAGAGACAAAGTGATGATGGAAGTGGACGTGGGTGTGACG  
TGAGCAGGGGCCATGAATGCCGCAGCCTTCAGATGCCAGAAAGGGAAAGGAATGGATTCCCC  
TGCCTGGAGCCTCCAAAAGAAACAGCCCTGCCACGCCTTGACTTGAGCCCATTGAAACTG  
ATCTTGAGCTCCTGGCCTCCAGAATTGCAGGAGAATAAATTTGTGTTGTTTTTAATGAAAAA  
AAA  
AAAG

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**FIGURE 40**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125200
><subunit 1 of 1, 290 aa, 1 stop
><MW: 32335, pI: 5.82, NX(S/T): 1
MPLLTLYLLLEFWLSGYSIATQITGPTTVNGLERGS�TVQCVYRSGWETYLKWWCRGAIWR
DCKILVKTSQSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT
VQVTIDPAPVTQEETSSSPTLTGHHLNDRHKLLKLSVLLPLIFTILLLLLVAASLLAWRM
MKYQQKAAGMSPEQVLQPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA
SLPKEDISYASLTILGAEDQEPTYCNMGHLSSHLPGRGPEEPTTEYSTISRP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-15

**Transmembrane domain:**

Amino acids 155-174

**N-glycosylation site:**

Amino acids 88-92

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 218-222

**Tyrosine kinase phosphorylation site:**

Amino acids 276-285

**N-myristoylation sites:**

Amino acids 30-36;109-115;114-120

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**FIGURE 41**

AAGAACACTGTTGCTCTTGGTGGACGGGCCAGAGGAATTCAGAGTTAAACCTTGAGTGCCT  
CGTCCGTGAGAATTCAGCATGGGAATGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTG  
CAAGATTGCCACTTGATGCCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCT  
GCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGA  
AAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCC  
GTGTGCAGGCGGTCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCG  
GTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAA  
GAACTGCAGAAATGAGGCTGGTTTATCTGCTGATCCGTATGTTTACAACCTGGACAGCATGGT  
CAGAGGACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGG  
AAACCTTTTCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTT  
GGTCAGTATTTCCAGAAATTGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCAATGT  
GACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATGTTT  
CCATCGCACAAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCTGTGTTTGTGACTATG  
TTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCTCAAAGATCTCCCCATTATGTT  
TGATGTCCTGATTCATGATCCTAGCCACTTCTCAATTATTCTACCATTAACATAAGTGGA  
GCTTCGGGGATAATACTGGCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTG  
CTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCC  
ACCGCCACCACCACCAGACCTTCAAACCCACCCCTTCTTTAGCAACTACTCTAAAATCTT  
ATGATTCAAACACCCACAGGACCTACTGGTGACAACCCCTGGAGCTGAGTAGGATTCCTGAT  
GAAAACCTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAAT  
CTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCT  
CCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCACGGAGGTCTGTACCATCATT  
TCTGACCCACCTGCGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGAT  
GTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCC  
TGGGGGATGACACAAGCCTGGCTCTCACGAGCACCCCTGATTTCTGTTCTTGACAGAGACCCA  
GCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGT  
CACTGTGATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTC  
CTGGGAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTT  
TTCCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA  
AATTTTCGACCTTGTTTCTGAAGCTCACTTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTG  
GCTATTAACCTTTTTTTTCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGA  
ATTTTTTATAGGTTAAATGTCATTTTATAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTC  
AGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTT  
TCACTTATAAAGTCTTAGGTAAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAG  
AAGCTACTATTGATTAGAGCCTAACCCAGGTAACTGCAAGAAGAGGCGGGATACTTTCAGC  
TTTCCATGTAAGTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTA  
ACTGAATCCCCTTCAATACACACTCATGAACCTTCTGATGGAACAATAACAGGCCCAAGCCT  
GTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAG  
TATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTA  
TTCCATGGACATTTAGTTAGTGCTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGT  
GTATATTTCCAAATTTTTGTACAGTCGCTGCACATATTTGAAATCATATATTAAGACTTTCC  
AAAGATGAGGTCCCTGGTTTTTTCATGGCAACTTGATCAGTAAGGATTTACCTCTGTTTGTA  
ACTAAAACCATCTACTATATGTTAGACATGACATTCTTTTTCTCTCTTCTGAAAAATAAA  
GTGTGGGAAGAGACA



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**FIGURE 42**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125214

&gt;&lt;subunit 1 of 1, 572 aa, 1 stop

&gt;&lt;MW: 63953, pI: 6.55, NX(S/T): 12

MECLYYFLGFLLLAARLPLDAAKRFHDVLGNERPSAYMREHNQLNGWSSDENDWNEKLYP  
VWKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLI FPRCQKEDANGNIVYEKNC  
RNEAGLSADPYVYNWTAWSESDSGENG TGQSHHNVFPDGKPFPHHPGWRWNFIYVFHTL  
GQYFQKLGRCSVRVSVNTANVTLG PQLMEVTVYRRHGRAYVP I AQVKDVYVVT DQIPVFV  
TMFQKNDNRNSSDETFLKDL PIMFDVLIHDP SHFLNYSTINYKWSFGDNTGLFVSTNHTVN  
HTYVLNGTFSLNLT VKAAAPGPCPPPPPPRPSKPTPSLATT LKSYDSNTPGPTGDNPLE  
LSRIPDENCQINRYGHFQATITIV EGILEVNIIQMTDVLMPVPWPPESSLIDFVVT CQGS I  
PTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLT LGDDTSLALTS  
TLISVPDRDPASPLRMANSALISVGCLAIFVTVISLLVYKKHKEYNPIENSPGNVVR SKG  
LSVFLNRAKAVFFPGNQEKDPLLKNQEFKGV S

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 496-516

**N-glycosylation sites:**Amino acids 93-97;134-138;146-150;200-204;249-253;275-279;  
296-300;300-304;306-310;312-316;459-463;467-471**N-myristoylation sites:**

Amino acids 91-97;147-153;290-296;418-424

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 496-507

**Cell attachment sequence:**

Amino acids 64-67

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**FIGURE 43**

GCATAGATGAATGTATCAGTGGATGGATAGTTGGCTAGATGGGTGGGTTGGTGGATGAATGG  
CAGAGCTTGCACCTGCCAGTCCATCTGACATCAAAGCCAGTGTCTCTAATGGTGACACCACC  
CTCCTCTGCAGCAGGAGGCAGAGCTGTGGGATGAATGAGGTTGCCAGGTCTCCCTTACCTA  
TCCTGGGTCCCCAGCTCCTTCTCACTCTCTTCCCTTGCAGCCTCGAAGCGGAGGATCCCTGT  
GTCCCAGCCGGGC**ATG**GCCGACCCCCACCAGCTTTTCGATGACACAAGTTCAGCCCAGAGCC  
GGGGCTATGGGGCCCAGCGGGCACCTGGTGGCCTGAGTTATCCTGCAGCCTCTCCACGCCC  
CATGCAGCCTTCCTGGCTGACCCGGTGTCCAACATGGCCATGGCCTATGGGAGCAGCCTGGC  
CGCGCAGGGCAAGGAGCTGGTGGATAAGAACATCGACCGCTTCATCCCCATCACCAAGCTCA  
AGTATTACTTTGCTGTGGACACCATGTATGTGGGCAGAAAGCTGGGCCTGCTGTTCTTCCCC  
TACCTAÇACCAGGACTGGGAAGTGCAGTACCAACAGGACACCCCGGTGGCCCCCGCTTTGAC  
GTCAATGCCCCGGACCTCTACATTCCAGCAATGGCTTTTCATCACCTACGTTTTGGTGGCTGG  
TCTTGCGCTGGGGACCCAGGATAGGTTCTCCCCAGACCTCCTGGGGCTGCAAGCGAGCTCAG  
CCCTGGCCTGGCTGACCCTGGAGGTGCTGGCCATCCTGCTCAGCCTCTATCTGGTCACTGTC  
AACACCGACCTCACCAACCATCGACCTGGTGGCCTTCTTGGGCTACAAATATGTCGGGATGAT  
TGGCGGGGTCCTCATGGGCCTGCTCTTCGGGAAGATTGGCTACTACCTGGTGCTGGGCTGGT  
GCTGCGTAGCCATCTTTGTGTTTCATGATCCGGACGCTGCGGCTGAAGATCTTGGCAGACGCA  
GCAGCTGAGGGGGTCCCGGTGCGTGGGGCCCGGAACCAGCTGCGCATGTACCTGACCATGGC  
GGTGGCGGCGGCGCAGCCTATGCTCATGTACTGGCTCACCTTCCACCTGGTGCGG**TGA**GCGC  
GCCCCGCTGAACCTCCCGCTGCTGCTGCTGCTGCTGGGGGCCACTGTGGCCGCCGAACTCATC  
TCCTGCCTGCAGGCCCAAGGTCCACCCTGTCTGGCCACAGGCACCGCCTCCATCCCATGTC  
CCGCCCAGCCCCGCCCCCAACCAAGGTGCTGAGAGATCTCCAGCTGCACAGGCCACCGCCC  
CAGGGCGTGGCCGCTGTTACAGAAACAATAAACCTGATGGGCATGGCAAAAAAAAAAAAAA  
AAA  
AAAAAGA

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**FIGURE 44**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125219
><subunit 1 of 1, 283 aa, 1 stop
><MW: 31175, pI: 7.51, NX(S/T): 0
MADPHQLFDDTSSAQSRGYGAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQ
GKELVDKNIDRFIPITKLKYYFAVD TMYVGRKLGLLFFPYLHQDWEVQYQQDTPVAPRFD
VNAPDLYIPAMAFITYVLVAGLALGTQDRFSPDLLGLQASSALAWLTLEVLAILLSLYLV
TVNTDLTTIDLVAFLGYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLKI
LADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 126-142;164-179;215-233

**N-myristoylation sites:**

Amino acids 54-60;141-147;156-162;201-207;205-211;209-215

**Amidation site:**

Amino acids 89-93

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**FIGURE 45**

GCTGAGCACCAACAGGAACTATTCCAGTGAAGAGCAAGTGCTGCCCCGACCCAGGACCCTGTG  
CCAGGCTGGCAGCCCTCCAGCTCCCTCCAGAGAGGAAACCTCTGTCTGGCTGAGGGTGGGAC  
TAGCTGGG**ATG**TCTCACTCCAGTTGCTCAGGTTACCCAGGAAGCTCCTCCGTGGAGTGGCC  
AGCCTGATTCTAGCCCTGTCTCTCTGGCAGCACATGCCACACCTGCCTGGGCCTTCTGCTC  
CCTGATGCTTGATGAGCCCCTGCTCCTCAATGTTTCTCAAAGACAGACCCCCCTGAGGCCAGC  
TTGAATGTGAAGACTGCTGAAGTCAGCTGGCTTCACTTGAGCTGCAGAAAAGGTGGCTGGGA  
TGGCCCAGGTGCACCCAGAGGCCCCAGCCCTTTGGCTGCCTTTGGGT**TGTA**CTTGGGTGT  
CTCTGAGGCCCTGCCAGAGCTGGGCCTGCGGGTGGTGGGCGGTCCGACCTCGGGCAGTCAGT  
GCTCCGCAGCCTCAGCACTGCATCCCAGACCCAGTGTCTCAGAGGGAAGAGCCAGCCTCCC  
TGCCTCATGGAACCAGGAGTCCCAAAAAGTCAGGAGCCTGGAGGCTCTGAAAGGAGCAGGGA  
TTCCATAGTGCGTGAAGCTGAAATAGGCGCCCTCCTGGGGAGCCCCCAGCAAAACTGTTTTT  
CATACCCACTCCCAGAACTGCCCCGCTCCAGCTCCAGCGCCAGCGCCAGCTGGTTGCCAGGC  
GTCATTGGAGAGGCCTGGCTGCCCCAGGGGCAGCAGGGAGTGGTGGACCTGTATGGGCTGGC  
AGGAGGCCATTGGCCATGCTGACAAGTGTACCTGCCTTCCTAGCCTGGAGCCACCCCTCAG  
GTGGCCTGCTTGACCTCCTATCCGGAGGTAGCCTGCCCCACCTGTAGGCAGAGGGGGCTCT  
TGCTTGAGGCCTGCACAGGAAGCAAGTATAGCCCCGGTGCCCCAGAGTGGGTTCACCTTAGC  
CCTGGCGAGATGGCCTGTCCTGAGATCTCTGCTCCCAGACCCACCATCTGGGGAGCACAGT  
CCTTAGGCTGCCTGGTCCAGGAAGGGGGTGGGCTCTGTCAGGAAACCTGGACTCTCAAGGC  
CCACCAGCCTCTCCGTGAGTGTTAGAAATCACAGATACAGTATATACTTAATTACACTACTC  
ACTACTCAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 46**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA128309
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10112, pI: 8.64, NX(S/T): 0
MSHSSCSGSPRKLLRGVASLILALSSLAHAATPAWAFCSLMLDEPLPPQCFSKTDPEAS
LNVKTAEVSWLHLSCRKGGWDGPGAPRGPSPLAAFGL
```

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-31

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**FIGURE 47**

TTCCGGGGCCCTGGCGTCTCGTCTCCTTACCCTGGGGCTACCCTTGCCCCGGTCCTACTGCCCG  
CGGTAAACCCGCCGCGAGCCGCCTCTCCCCTCCCCGCCCGACTCAACCCTGCCCTCCCCCGT  
GCTTTGCAGACGCCGCCCGGGGGCCAGGCGGCTGATGCGTGTGGGCCTCGCGCTGATCTTG  
GTGGGCCACGTGAACCTGCTGCTGGGGGCCGTGCTGCATGGCACCGTCCTGCGGCACGTGGC  
CAATCCCCGCGGCGCTGTCACGCCGAGTACACCGTAGCCAATGTCATCTCTGTGCGGCTCGG  
GGCTGCTGAGCGTTTCCGTGGGACTTGTGGCCCTCCTGGCGTCCAGGAACCTTCTTCGCCCT  
CCTGCGACTGGGTCTGCTGGCACTAGCTCTGGTGAACCTGCTCTTGTCGTTGCCTGCTC  
CCTGGGCCTCCTTCTTGCTGTGTCACTCACTGTGGCCAACGGTGGCCGCCGCCCTTATTGCTG  
ACTGCCACCCAGGACTGCTGGATCCTCTGGTACCCTGGATGAGGGGGCCGGGACATACTGAC  
TGCCCCCTTTGACCCCAACAAGAATCTATGATACAGCCTTGGCTCTCTGGATCCCTTCTTTGCT  
CATGTCTGCAGGGGAGGCTGCTCTATCTGGTTACTGCTGTGTGGCTGCACTCACTCTACGTG  
GAGTTGGGCCCTGCAGGAAGGACGGACTTCAGGGGCAGCTAGAGGAAATGACAGAGCTTGAA  
TCTCCTAAATGTAAAAGGCAGGAAAATGAGCAGCTACTGGATCAAAATCAAGAAATCCGGGC  
ATCACAGAGAAGTTGGGTTTAGGACAGGTGCTGTTCCGAGACTCAGTCCTAAAGGGTTTTTT  
TTCCCACTAAGCAAGGGGCCCTGACCTCGGGATGAGATAACAAATTGTAATAAAGTAACTTC  
TCTTTTCTTCTAAAAA

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## FIGURE 48

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129535
><subunit 1 of 1, 222 aa, 1 stop
><MW: 23566, pI: 6.70, NX(S/T): 0
MRVGLALILVGHVNLLLGAVLHGTVLRHVANPRGAVTPEYTVANVISVGSGLLSVSVGLV
ALLASRNLLRPPLHWVLLALALVNLLLSVACSLGLLAVSLTVANGGRRLIADCHPGLLD
PLVPLDEGPGHTDCPFDPTRIIDTALALWIPSLMLSAGEAALSGYCCVAALTLRGVGPCR
KDGLOGQLEEMTELESPKCKRQENEQLLDQNEIRASQRSWV
```

### Important features of the protein:

#### Signal peptide:

Amino acids 1-18

#### Transmembrane domain:

Amino acids 44-60;76-96

#### N-myristoylation sites:

Amino acids 94-100;175-181

#### Amidation site:

Amino acids 106-110

#### Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 81-92

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**FIGURE 49**

CGTCAGTCTAGAAGGATAAGAGAAAGAAAGTTAAGCAACTACAGGAAATGGCTTTGGGAG  
TTCCAATATCAGTCTATCTTTTATTCAACGCAATGACAGCACTGACCGAAGAGGCAGCCG  
TGACTGTAACACCTCCAATCACAGCCCAGCAAGCTGACAACATAGAAGGACCCATAGCCT  
TGAAGTTCTCACACCTTTGCCTGGAAGATCATAACAGTTACTGCATCAACGGTGCTTGTG  
CATTCACCATGAGCTAGAGAAAGCCATCTGCAGGTGTTTTACTGGTTATACTGGAGAAA  
GGTGTGAGCACTTGACTTTAACTTCATATGCTGTGGATTCTTATGAAAAATACATTGCAA  
TTGGGATTGGTGTGGATTACTATTAAGTGGTTTTCTTGTTATTTTTTACTGCTATATAA  
GAAAGAGGTATGAAAAAGACAAAATATGAAGTCACTTCATATGCAATCGTTTGACAAATA  
GTTATTCAGGCCCTATAATGTGTCAGGCACTGACATGTAAAATTTTTTTAATTAAAAAAG  
AGCTGTAATCTGGCAAAAAGTTTCTATGTAATATTTTTCATGCCTTTTCTCATAAACCCA  
GACGAGTGGTAAAAATTTGCCTTCAGTTGTAATAGGAGAGTTCAAACGTACAGTCTCCCT  
TCAACCTATCTCTGTCTGCCCATATCAAAATTATAAATGAGGAGGACAGCAGGCCCAAG  
AAAGTAGGGACTAAGTATGTCTTGTTCAAAATTGTATATTCAGTGACTTACACTATGCCT  
AGCACACAACACACACTGAGTAAATATTTGTTGAGTGAAATAAAATCAAGAAACAAGTAA  
AAACTGA



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## FIGURE 50

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129549
><subunit 1 of 1, 133 aa, 1 stop
><MW: 14792, pI: 5.97, NX(S/T): 0
MALGVPISVYLLFNAMTALTEEA AVTVTPPITAQQADNIEGP IALKFSHLCLEDHNSYCI
NGACAFHHELEKAICRCFTGYTGERCEHLTLTSYAVDSYEKYIAIGIGVGLLLSGFLVIF
YCYIRKRYEKDKI
```

**Important features of the protein:**

**Signal peptide:**

1-20 (weak)

**Transmembrane domain:**

103-117

**N-myristoylation site.**

4-10;106-112;110-116

**EGF-like domain cysteine pattern signature.**

75-87

**Integrins beta chain cysteine-rich domain proteins**

66-88

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**FIGURE 51**

GGCTCGAGCTTGGCTCTCAGACCATCCTGGTGGAAGAAACACTAGCAGTCTGCCCAATCTGA  
ATGCAAATCCAGAATAATCTTTCTTTTGTGTGTTACACAGTTATGAGTGCAATTTTAAATG  
GCTGCTACTCTACAGCCTGCCTGCCTTATGCTTTCTCCTGGGCACGCAGGAAAGTGAGAGCT  
TCCACTCCAAAGCAGAGATCCTAGTGACACTAAGTCAGGTAATAATCTCTCCAGCTGGACCT  
CATGCACTCACATGGACAACACACTTCTCTCCTTCAGTGATCATCATCCTTGTACCATGTTG  
GTGGCATGCTGTAATCGTGACTCAACATCCGGTTGCCAATTGCTATGTAACAAACCACCTCA  
ACATTCAAGTGGCTTGAATTGAAAGCAGGGTCTTGAAGAGATATTTGCACATTTTCATCCTCCC  
AGCAGCATTATTCCACAACAGCCAATAGGCAGAAGCAACCCAATGTCCAACCATAGATGAGTG  
GATAACCAAAATGTAGTCCATCCATACAATGAAATATGATTCAGCCTTAACAAGGAAGGAAG  
TCCCGCCACGTGCTACAACATGGATGGACCTTGAGGACACTATGCTAAGTGAAGTAAGCCAG  
GCACAAAAGGACAAATACTCTATGATTCCATTTTATAGGGTACCAAAGAGAATCAAACCTCAC  
AGAGATAGAAAGTAGACTGGGGTGGCCAGGGACTCGGGGAGAGAGGAAAGGGCAGTTATTGT  
TTAAAAGGTACAGAGTTTCAGTTTGGGAAGATGAAAATGTTCTGGAAACGGTTAATGGTGAT  
TTTACATTGTTTATGTTACCACGATTTGTAAAAGAGCAGCTGCGCTGAGAATGAGCATGCTT  
GTCATTGGCAGCTCTCTGAGATTTTCAGTGCCTCTTACTGGCTTGTTAAGAAGACGGCAAAA  
AA

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**FIGURE 52**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129580  
><subunit 1 of 1, 114 aa, 1 stop  
><MW: 12886, pI: 7.04, NX(S/T): 0  
MQIQNNLFFCCYTVMSAIFKWLLLYSLPALCFLLGTOESESFHSKAEILVTLSQVIISPA  
GPHALTWTTTHFSPSVIIILVPCWWHAVIVTQHPVANCYVTNHLNIQWLELKAGS

**Important features of the protein:****Signal peptide:**

Amino acids 1-33

**Transmembrane domain:**

Amino acids 71-86

**N-myristoylation site:**

Amino acids 35-41

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**FIGURE 53**

TTTTGAAATGGTTTATGACCTCTTCCCCACTTCCCCGCTTGCTTTGCTCATTAGTGTTTCCTA  
GGTGGCTGCTGGGTGACGGGCTTTTCATCATCTCTGATGTGGGCCAGTGCGAAAGAGCAGCT  
GCAACATCTGTTTCTAATTGGGTCGTGCCTTTATAAATACTTCTTGCCTATTTGTCACATTG  
CTTCCCTCCCACCCTGTCTTCCTTGGAGTACTGCAGAATCTGTAAGCGTCCCTGGAATGCAC  
ACGTGGACCTTGTCAATCCCAAACAGACTTTCTGCTGGTCAGCACTTTGTAATGTTCCGGCTG  
TTACAGGCATTAGTCACTTGTGCTCAGAGAGAGACTGTGGTCTTTGGAACTGAAGAAAATGTC  
TTTTTTGTTGTTGTTAATTCTTGGCATCCAGTTAGATTTAACTTCTCAAGAGTTTACACAGA  
CTTTTAGAAAAACATTCTGTCTCTAAGAAAAAAGTGCTCTAGCTTTGTACAGTTTTTGGATT  
TTCACACTTGGTGGTTGTTTGCTGAAATGCTGTTTGCTAGTGATTCCCCCTCCTCCCCCTAT  
CTGGGGTTGTAAGCAGCTCTGGGGCTCTGTTCACTTCGGATACCTGTTTCTGGGGACTGCTT  
TTCAACAGCGTTTTTCTAAGGGCATATGAGAAATTTAATTTCTGATGGAATGAAGGTGAAA  
CTCTAGTCCCAGGTAAACCTGGGTAGGCTGTAGAGACAGAAAGGGGGCTGCAGGTCTAGGTG  
GAAGAACGAGAACGAATGCAGCATGGTATTTCCAGGCCTTTTAGATTTCGGCTTCATCCACAA  
CCAATGTGAGTTCTTATCTGCAAAGCGGGCCTAAGTGTAATGGAGGGAAGGTGGGCCAGGCA  
CCAGGGTCCTGGGTCTCCCGCGCCTCACTCTGTCTCCACCTGGCCCATGCATAAAGAACAC  
TAGTCAAGTAGCCATTGTACCTGTTTCTTATCTGAAAATGAGAAGGTGGAGAGTATGACT  
TCTGTTGAAACAACAAGGCGCTTACAAATTTTGGTGAAGTCGAATGAGGGCAGCGTTAAGAG  
AAATATCAAAGTTAGTCATTGGATTTCAAGGGCTTAGGGATGGAAACCAGCTGGTAGTAGACT  
GGTTGTAGTTATGTCCAAAGGGCAGAGTGGGAAAAATTTGGCCGAAAAGAGTGTGGTGGGTG  
ACCAGCAAATGTTAGAGGTATACATCAGGGCACAGAGGAGAAAAGCTAACATGATACTGATG  
ACTTCAAGTCTTCACTGTCCAATTCAGAGGATAGGGGAGGGTTTAAGCTGATTAAACAGTGG  
GCTTTTTTTCTCCTGCAAGAGGGTGGAGGTCTATAACTGTGCAGATTTTATCAGATGCATGC  
TAATACATGTTATTCTGGGGGACTCTCTTATACCTTGAAGTAGACATTGCTGCTATTTGCGT  
GAAAAAATAGGAGGACTTATTTGAATTGAGAATGGGGATAGGCTGAGTTCCACCGAGATGT  
TGGCTTAGAGATGCCTGGGCCATGCTGTACAGTAGGAAGCCCAGCAGAGGAGATTGGGCTGT  
GTGGGTCATGACAAAGGGAGTTGTTAGCTTATGGTTGGCTATTAAAGTCATGGGCAAGGATG  
GGCAAGAAAAGTGTGTAAATGAGCTGACAAAAGATAAATATGTTAATTA

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**FIGURE 54**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129794
><subunit 1 of 1, 102 aa, 1 stop
><MW: 11382, pI: 8.72, NX(S/T): 0
MTSSPLPRLCSLVFLGGCWVTGFSSSLMWASAKEQLQHLFLIGSCLYKYFLPICHIASL
PPCLPWSTAESVSVPGMHTWTLSFPNRLSAGQHFVMFGCYRH
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**N-myristoylation site:**

Amino acids 18-24

**Prokaryotic membrane lipoprotein lipid attachment sites:**Amino acids 9-20;36-47;  
89-100

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**FIGURE 55**

ACACTGGCCAAACACTCGCATCCCAGGGCGTCTCCGGCTGCTCCCATTGAGCTGTCTGCTCG  
CTGTGCCCCGCTGTGCCTGCTGTGCCCCGCGCTGTGCGCCGCTGCTACCGCGTCTGCTGGACGCG  
GGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCCAGCTCTGCCCCG  
AGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTC  
CTGGGTGGTGTTCATCCCCTTGGGGCTGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCT  
GCCCCAACGTCACTCTCTTAGAGGAGCTGCTCAGCAAATACCAGCACAAAGAGTCTCACTCCC  
GGGTCCGCAGAGCCATCCCCAGGGAGGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTT  
CGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACATGACCTGGGATGACGAACCTGGA  
GAAGTCTGCTGCAGCGTGGGCCAGTCAGTGCATCTGGGAGCACGGGCCACCAGTCTGCTGG  
TGTCCATCGGGCAGAACCTGGGCGCTCACTGGGGCAGGTATCGCTCTCCGGGGTTCCATGTG  
CAGTCTTGGTATGACGAGGTGAAGGACTACACCTACCCCTACCCGAGCGAGTGCAACCCCTG  
GTGTCCAGAGAGGTGCTCGGGGCCATATGTGCACGCACTACACACAGATAGTTTGGGCCACCA  
CCAACAAGATCGGTTGTGCTGTGAACACCTGCCGGAAGATGACTGTCTGGGGAGAAGTTTGG  
GAGAACGCGGTCTACTTTGTCTGCAATTATTCTCCAAAGGGGAACGGATTGGAGAAGCCCC  
CTACAAGAATGGCCGGCCCTGCTCTGAGTGGCCACCCAGCTATGGAGGCAGCTGCAGGAACA  
ACTTGTGTTACCGAGAAGAAACCTACACTCCAAAACCTGAAACGGACGAGATGAATGAGGTG  
GAAACGGCTCCCATTCCTGAAGAAAACCATGTTTGGCTCCAACCGAGGGTGATGAGACCCAC  
CAAGCCCAAGAAAACCTCTGCGGTCAACTACATGACCCAAGTCGTCAGATGTGACACCAAGA  
TGAAGGACAGGTGCAAAGGGTCCACGTGTAACAGGTACCAGTGCCGAGCAGGCTGCCTGAAC  
CACAAGGCGAAGATCTTTGGAAGTCTGTTCTATGAAAGCTCGTCTAGCATATGCCGCGCCGC  
CATCCACTACGGGATCCTGGATGACAAGGGAGGCCTGGTGGATATCACCAGGAACGGGAAGG  
TCCCCTTCTTCGTGAAGTCTGAGAGACACGGCGTGCAGTCCCTCAGCAAATACAAACCTTCC  
AGCTCATTCATGGTGTCAAAGTGAAAGTGCAGGATTTGGACTGCTACACGACCGTTGCTCA  
GCTGTGCCCCGTTTGAAGGCCAGCAACTCACTGCCCCAAGAATCCATTGTCCGGCACACTGCA  
AAGACGAACCTTCCTACTGGGCTCCGGTGTGTTTGAACCAACATCTATGCAGATACCTCAAGC  
ATCTGCAAGACAGCTGTGCACGCGGGAGTCATCAGCAACGAGAGTGGGGGTGACGTGGACGT  
GATGCCCCGTGGATAAAAAGAAGACCTACGTGGGCTCGCTCAGGAATGGAGTTCAGTCTGAAA  
GCCTGGGGACTCCTCGGGATGGAAAGGCCTTCCGGATCTTTGCTGTGAGGCAGTGAATTTCC  
AGCACCAGGGGAGAAGGGGCGTCTTCAGGAGGGCTTCGGGGTTTTGCTTTTATTTTATTTT  
GTCATTGCGGGGTATATGGAGAGTCA

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**FIGURE 56**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131590
><subunit 1 of 1, 497 aa, 1 stop
><MW: 55906, pI: 8.43, NX(S/T): 4
MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLEELLISKYQHNEHSRVRRAIPREDKEEIL
MLHNKLRGQVQPQASNMEYMTWDDELEKSAAAWASQCIWEHGPTSLLVSIGQNLGAHWGR
YRSPGFHVQSWYDEVKDYTYPPSECNPWCPCRCSGPMCTHYTOIVWATTNKIGCAVNTC
RKMTVWGEVWENAVYFVCNYSKGNWIGEAPYKNGRPCSECPPSYGGSCRNNLCYREETY
TPKPETDEMNEVETAPIPEENHVWLQPRVMPRTKPKKTSAVNYMTQVVRCDTKMKDRCKG
STCNRYQCPAGCLNHNKAKIFGSLFYESSSSICRAAIHYGILDDKGGGLVDITRNGKVPFFV
KSERHGVQSLSKYKPPSSFMVSKVKVQDLDCYTTVAQLCPFEKPATHCPRIHCPAHCKDE
PSYWAPVFGTNIYADTSSICKTAVHAGVISNESGGDVDVMPVDKKKTYVGSLRNGVQSES
LGTPRDGKAFRIFAVRQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-glycosylation sites:**

Amino acids 27-31;41-45;451-455

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 181-185;276-280;464-468

**Tyrosine kinase phosphorylation site:**

Amino acids 385-393

**N-myristoylation sites:**Amino acids 111-117;115-121;174-180;204-210;227-233;300-306;  
447-453;470-476**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

Amino acids 195-207

**SCP-like extracellular protein:**

Amino acids 56-208

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**FIGURE 57**

GCACGAGGCCAAACACAGCAGCCTCAACATGAAGGTGGTTATGGTCCTCCTGCTTGCTGCCC  
TCCCCCTTTACTGCTATGCAGGTTCTGGTTGCGTTCTTCTGGAGAGCGTCGTGGAAAAGACC  
ATCGATCCATCGGTTTCTGTGGAGGAATACAAAGCAGATCTTCAGAGGTTTCATCGACACTGA  
GCAAACCGAAGCAGCTGTAGAGGAGTTCAAGGAGTGCTTCCTCAGCCAGAGCAATGAGACTC  
TGGCCAACTTCCGAGTCATGGTGCATACGATATATGACAGCCTTTACTGTGCTGCGTATTAA  
CTGTCACAAGAACTTTGGCTCAGAGGAATCCAGACGATGCTCACAACCCGACTGTGGACTGG  
CAGAAATCTCAACTTTTCCTTTTGACTTTCCCCTTTGATCAGTAATATGGAAGACGTTGTTG  
AAACCTGAAGTATAGTTAATTTAAATAAACCCACTGCAAGAAAAAAAAAAAAA



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**FIGURE 58**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA135173
><subunit 1 of 1, 93 aa, 1 stop
><MW: 10456, pI: 4.37, NX(S/T): 1
MKVVMVLLLLAALPLYCYAGSGCVLLESVVEKTIDPSVSVVEEYKADLQRFIDTEQTEAAVE
EFKECFLSQSNETLANFRVMVHTIYDSLYCAAY
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 12-23

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**FIGURE 59A**

CAAGTCCGTTGAGGCTGCCAGGCGAGTCAGGTCTCTCTGGACCTCGCCTGACTCGGCTGGGC  
TGTGCCTGAAATTGACCCAGCTCCACCATACTCCTTGATTATGAGAGAAAACAAGGAGTAAGCT  
CAAAGCGGCTGCAATCTTCCGGCCGAGCCAGTCTAAGGGGCGGCGCGGGGCTCCCTCGCC  
CGGGAGCCGGAGGTAGAGGAGGAGGTGGAAAAGTCGGTCCTAGGCGGCGGGAAACTGCCAAG  
GGGCGCCTGGAGGTCCTCCCCGGGGAGGATCCAAAGTCTGAAAGAGCGAAAAGGCTTGGAGC  
TAGAGGTGGTGGCCAAGACCTTTCTTCTCGGCCCTTCCAGTTCGTCCGTAATTCCCTGGCG  
CAGCTCCGGGAAAAGGTGCAGGAAGTGCAGGCGCGGCGGTTCTCCAGCAGAACCCTCTCGG  
CATCGCTGTCTTTGTGGCAATTTTACATTGGTTACATTTAGTAACACTTTTTGAAAATGATC  
GTCATTTCTCTCACCTCTCATCTTTGGAACGGGAGATGACTTTTCGCACTGAAATGGGACTT  
TATTATTCATACTTCAAGACCATTATTGAAGCACCTTCGTTTTTGAAGGACTGTGGATGAT  
TATGAATGACAGGCTTACTGAATATCCTCTTATAATTAATGCAATAAAACGCTTCCATCTTT  
ATCCAGAGGTAATCATAGCCTCCTGGTATTGCACATTCATGGGAATAATGAATTTATTTGGA  
CTAGAACTAAGACCTGCTGGAATGTCACCAGAATAGAACCCTTTAATGAAGTTCAAAGCTG  
TGAAGGATTGGGAGATCCTGCTTGCTTTTATGTTGGTGTAATCTTTATTTTAAATGGACTAA  
TGATGGGATTGTTCTTCATGTATGGAGCATACTGAGTGGGACTCAACTGGGAGGTCTTATT  
ACAGTACTGTGCTTCTTTTTCAACCATGGAGAGGCCACCCGTGTGATGTGGACACCACCTCT  
CCGTGAAAGTTTTTCTATCCTTTTCTTGACTTCAGATGTGTATTTTAACTTTGATTCTCA  
GGACCTCAAGCAATGATAGAAGGCCCTTCATTGCACTCTGTCTTTCCAATGTTGCTTTTATG  
CTTCCCTGGCAATTTGCTCAGTTTATACTTTTTACACAGATAGCATCATTATTTCCCATGTA  
TGTTGTGGGATACATTGAACCAAGCAAATTTTCAAGATCATTATATGAACATGATTTAGTT  
ACCCTTAGTTTTTATTTGATGTTTGGAAATTCATGTACTTATCTTCTTATTATTCTTCATC  
TTTGTTAATGACGTGGGCAATAATTCTAAAGAGAAATGAAATTCAAAACTGGGAGTATCTA  
AACTCAACTTTTTGGCTAATTCAAGGTAGTGCCTGGTGGTGTGGAACAATCATTTTGAAATTT  
CTGACATCTAAAATCTTAGGCGTTTCAGACCACATTCGCCTGAGTGATCTTATAGCAGCCAG  
AATCTTAAGGTATACAGATTTTGATACTTTAATATATACCTGTGCTCCCGAATTTGACTTCA  
TGGAAAAAGCGACTCCGCTGAGATACACAAAGACATTATTGCTTCCAGTTGTTATGGTGATT  
ACATGTTTTATCTTTAAAAGACTGTTTCGTGATATTTTCATATGTTTTAGCTACAAACATTTA  
TCTAAGAAAACAGCTCCTTGAACACAGTGAGCTGGCTTTTACACATTGCAGTTGTTAGTGT  
TTACTGCCCTTGCCATTTTAAATTATGAGGCTAAAGATGTTTTTGACACCCGCACATGTGTGTT  
ATGGCTTCCTTGATATGCTCTCGACAGCTCTTTGGCTGGCTTTTTTCGCAGAGTTCGTTTTGA  
GAAGGTTATCTTTGGCATTTTTAAACAGTGATGTCAATACAAGGTTATGCAAACCTCCGTAATC  
AATGGAGCATAATAGGAGAATTTAATAATTTGCCTCAGGAAGAACTTTTACAGTGGATCAAA  
TACAGTACCACATCAGATGCTGTCTTTGCAGGTGCCATGCCTACAATGGCAAGCATCAAGCT  
GTCTACACTTCATCCCATTGTGAATCATCCACATTACGAAGATGCAGACTTGAGGGCTCGGA  
CAAAAATAGTTTATTCTACATATAGTCGAAAATCTGCCAAAGAAGTAAGAGATAAATTGTTG  
GAGTTACATGTGAATTATTATGTTTTAGAAAGAGGCATGGTGTGTTGTGAGAATAAGCCTGG  
TTGCAGTATGCTTGAATCTGGGATGTGGAAGACCCTTCCAATGCAGCTAACCCTCCCTTAT  
GTAGCGTCTGCTCGAAGACGCCAGGCCTTACTTCACCACAGTATTTTCAGAATAGTGTGTAC  
AGAGTATTAAAGGTTAACTGAGAAGGATACTACCCATTTTACTATGGCACAAATGCCGTGTGT  
CAAAAACAATCACCCCTTTGGCTTATTCACATTAATAAAAATCACAAGCTTTAATAACAGACA  
CTTAAAAATAAGATAAAAATGGATTGGAATTTTTCTGATTACTAAAAGGTAAATTACTTTT  
CTGTTTCATTGAATGTCAGCCTTATTAAGCTTGTATATAAGTTATTAAATCATTTCATGTAT  
ACTGCATAAACAAATGTTTCATTTTCAAGATTTTAAAGAGAAATGTATATAAAGAACMATGATT  
TTAATAATCAGGGGTATGTAAGTCCTTTTTTCATCCAAGTGAATTGCTTCAGATTTTCT  
CTAGTACCAGAGGGTACCTCCTCAAACCTTTTGAACCACTTAAGGCAGAAGAATGCAAGCTC  
TGAAATGACATCCTTAAAATGCTGATACTGGTCACAGCCTCTTTACCTCTGTGAGGAAATG  
TAACAGTGTGTCTTTTAAAGGTGTTTTTATTTTACCAGCCCTTAAGAAAGATCTCTAATACCT  
TTTAATACTTTTTTTTTAATAATTTCAAGTTGAAGTGTTTTTTAAAACACTTTGTTTTGTAAT  
GTTTTGAATCTCTTGAGATGTGTTTACCCCACTAGATACATATTTGCCACTGGTTAGTTCTC  
CATCTAAGCTCAAGAGGTTATTCATCTCTTTTAGATTCCAGTGGCTTTTCTTTTAAACATCC  
AGGTAAAACAGAACTGCTATGGTATACAACCAAGTTTTGGGGTTAAACATAATCAGAAAAG

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**FIGURE 59B**

AAAATCCAGTTAAATTTATGAAGTGAGATTTTCAGATCCTAGATCTTGAATAAAGGAAAGGT  
CTTTTCATCTTGATGGCCCCAAAGCTTGTTGGTCATGGTCTTTATTTCTGGCCACTATCTTC  
TTAAATAATATATTTTTTAAGCCCTCATTATTTTTGGTTTTGGGTGAGGAAAGTCATGTTTT  
CTAAGTCCTCTCCCCTAATAAAACCTACCCAACAATAGTGCTTTGAAAAGTGGTAGTTATCT  
TGAAGATACTCTTGCCAAATGCAAAGATAAACATTCTTTTTGTCTGCTTTATAAATATGAAA  
TATGCCAGATCTATAGTATTTTAATGTGCATCTACTTTAAATGAGTCATCTTGGGGTTTTTA  
TAATTCCTTATGTTCTTGCCCCCTACACTTGAAATAACAAAATGCCTTAATTTTTATGGAT  
TAGTTCTCTTATAGTAGACAGGCAGCTATATGCAGCAAACCAATAAAGTTATTTTTCAACT  
TTCATAGTTGTAAAATATCTTATAACCAGAATACAAAACAGCTAAGAAAACATGCCACATTTTTAT  
TTTAGCATTTTCAAATAATTTGTTTTTGGTGTAAGCACAGGATAAAAAAGGAGAGCGTCAAA  
GAAAAGAGACATAACACCTAACATTCATAAAAATTAACAAAGTATATTTTGGATGATGTTTT  
TACAGGAAATATTTTAAATAAGTTGGTAGAACTTTTAAAATGGTACTGTATTAGCTAATAAA  
ATATTCAGTACAAATATATGTTTGGATTTATGCATTAAAAAACTAATAAAATTATTTCCAAC  
TTTA

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**FIGURE 60**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA138039
><subunit 1 of 1, 758 aa, 1 stop
><MW: 87354, pI: 9.36, NX(S/T): 1
MRKQGVSSKRLQSSGRSQSKGRRGASLAREPEVEEEVEKSVLGGGKLPRGAWRSSPGRIQ
SLKERKGLELEVVAKTFLLGPFQFVRNSLAQLREKVQELQARRFSSRTTLGIAVFVAILH
WLHLVTLFENDRHFHSHLSSLEREMTFRTEMGLYYSYFKTIEAPSFLEGLWMIMNDRLTE
YPLIINAIKRFHLYPEVIIASWYCTFMGIMNLFGLTETKTCWNVTRIEPLNEVQSCEGLGD
PACFYVGVI FILNGLMMGLFFMYGAYLSGTQLGGLITVLCFFFNHGEATRVMWTPPLRES
FSYPFLVLQMCILTLILRTSSNDRRPFIALCLSNVAFMLPWQFAQFILFTQIASLFPMYV
VGYIEPSKFKQIIYMNMISVTLSFILMFGNSMYLSSYYSSSLMTWAILKRNEIQKLGV
SKLNFWLIQGSAAWCGTIILKFLT SKILGVS DHIRLSDLIAARILRYTDFDTLIYTCAPE
FDFMEKATPLRYTKTLLLPVVMVITCFIFKKTVRDISYVLATNIYLRKQLLEHSELAFT
LQLLVFTALAILIMRLKMFLTPHMCVMASLICSRLFGWLFRRVRFEKVIFGILTVMSTQ
GYANLRNQWSIIIGEFNNLPQEELQWIKYSTTS DAVFAGAMPTMASIKLSTLHPVNHHPH
YEDADLRARTKIVYSTYSRKS AKEVRDKLLELHVNYVLEEAWCVVRTKPGCSMLEIWDV
EDPSNAANPPLCSVLLEDARPYFTTVFQNSVYRVLKVN
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 109-124;197-213;241-260;266-283;302-315;336-356;  
376-391;430-450;495-509;541-560;584-599;634-647

**N-glycosylation site:**

Amino acids 222-226

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 102-106

**Tyrosine kinase phosphorylation site:**

Amino acids 511-519

**N-myristoylation sites:**

Amino acids 24-30;50-56;151-157;254-260;264-270;269-275;  
273-279;639-645

**Amidation site:**

Amino acids 20-24

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**FIGURE 61**

GGCGCGGCCACATCCTTTAAATATGGTCTTTCTTGGGCGCGCGGACAATGTGAGGAGTGGG  
GTGGAGCGTGTGTGGTGTGTGGCTGCGGCCTGGGCAAGAGCCGCCGCGGACCATGAGCTGAG  
TAAGTTCTGGAGGGATCCTGCCTCTTGGAGCCTTCGCAGCCAGGCAGCTGTGAACTGTGAGC  
TAGAGTGAAGCAGAAATCTAGGAAGATGAGCTCCAAGATGGTCATAAGTGAACCAGGACTGA  
ATTGGGATATTTCCCCCAAAAATGGCCTTAAGACATTTTTCTCTCGAGAAAATTATAAAGAT  
CATTCCATGGCTCCAAGTTTAAAAGAACTACGTGTTTTATCCAACAGACGTATAGGAGAAAA  
TTTGAATGCCTCAGCAAGTTCTGTAGAAAATGAGCCGGCAGTTAGTTCAGCAACTCAAGCAA  
AGGAAAAAGTTAAAACCACAATTGGAATGGTTCTTCTTCCAAAACCAAGAGTTCCTTATCCT  
CGTTTCTCTCGTTTCTCACAGAGAGAGCAGAGGAGTTATGTGGACTTGTTGGTTAAATACGC  
AAAGATTTCCTGCAAATTCCAAAGCTGTTGGAATAAATAAAAAATGACTACTTGCACTACTTGG  
ATATGAAAAAACATGTGAACGAAGAAGTTACTGAGTTCCTAAAGTTTTTGCAGAATTCTGCA  
AAGAAATGTGCGCAGGATTATAATATGCTTTCTGATGATGCCCGTCTCTTCACAGAGAAAAT  
TTTAAGAGCTTGCAATTGAACAAGTGAAAAAGTATTCAGAATTCTATACTCTCCACGAGGTCA  
CCAGCTTAATGGGATTCTTCCCATTCAGAGTAGAGATGGGATTAAAGTTAGAAAAAACTCTT  
CTCGCATTGGGCAGTGTAATAATGTGAAAACAGTATTTCCCTCAATGCCTATAAAGTTGCAG  
CTGTCAAAGGACGATATAGCTACCATTGAAACGTGAGAACAACAGCTGAAGCTATGCATTA  
TGATATTAGTAAAGATCCAAATGCAGAGAAGCTTGTTTCCAGATATCACCTCAGATAGCTC  
TAACTAGTCAGTCATTATTTACCTTATTAATAATCATGGACCAACGTACAAGGAACAGTGG  
GAAATTCAGTGTGTATTCAAGTAATACCTGTTGCAGGTTCAAACCAAGTTAAAGTAATATA  
TATTAATTCACCACTTCCCCAAAAGAAAATGACTATGAGAGAGAGAAAATCAAATCTTTCATG  
AAGTTCATTAAAAATTTATGATGTCCAAAACACATCTGTTCCAGTCTCTGCAGTCTTTATG  
GACAAACCTGAAGAGTTTATATCTGAAATGGACATGTCTGTGAAGTCAACGAGTGCCGAAA  
AATTGAGAGTCTTGAAAACCTTGATTTTGATTTTGATGATGATGTCACAGAAGTTGAACTT  
TTGGAGTAACCACCACCAAGTATCAAATCACCAAGTCCAGCAAGTACTTCCACAGTACCT  
AACATGACAGATGCTCCTACAGCCCCCAAAGCAGGAAGTACAAGTGTGGCACCAAGTGCACC  
AGACATTTCTGCTAATCTAGAAAGTTTATCTCAGATTCTGATGGAACAATTGCAAAAGGAGA  
AACAGCTGGTCACTGGTATGGATGGTGGCCCTGAGGAATGCAAAAATAAAGATGATCAGGGA  
TTTGAATCATGTGAAAAGGTATCAAATCTGACAAGCCTTTGATACAAGATAGTGACTTGAA  
AACATCTGATGCCTTACAGTTAGAAAATCTCAGGAAATTGAACTTCTAATAAAAATGATA  
TGACTATAGATATACTACATGCTGATGGTGAAGACCTAATGTTCTAGAAAACCTAGACAAC  
TCAAAGGAAAAGACTGTTGGATCAGAAGCAGCAAAAACCTGAAGATACAGTTCTCTGCAGCAG  
TGATACAGATGAGGAGTGTTAATCATTGATACAGAATGTAAAAAAACCAGTTATAACAGTG  
TTTAAATTTAGATAAGTTTGAGGGGAAAATAATCAGTAGGCAAGAGGAACATTTTTCTGTAGT  
AGCTAGAGTGCTTTGAAAAAATGTGTTGGCTATGTGAAGGAATATTTCAACTAAAATGGAAT  
GGTATGCTTTTCACCCTTAAAGTTTGAGGAGGATCTTGATATGTTTTAACATTATCATGGCA  
GGGAAATATATAAGAAGAAAAATATTTTTACATTAAACCTTTTCTAAAAATGTAAATAGA  
AAAATAAATTTGGTTTTTTTATCAAGAACAACACTTATCGTTATGTATTGTGTTAGTTATATTG  
CCAGTCTGTTGCGACTGACTCAAAAAGTTAAATGTTGCCACTGCTGAAGATGATTATGAGCA  
TCGCAAACTTTGTTTCTGACCCATTTTGACAGTTTTTATATACTCCTTTAAATGATGAATG  
TTACAGGTTAATAAAGTTAATACCTTTAAA

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**FIGURE 62**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139540
><subunit 1 of 1, 592 aa, 1 stop
><MW: 66453, pI: 5.42, NX(S/T): 3
MSSKMVISEPGLNWDISPKNGLKTFFSRENYKDHSMAPSLKELRVLSNRRIGENLNASAS
SVENEPAVSSATQAKEKVKTITIGMVLLPKPRVPYPFRFSRFSQREQRSYVDLLVKYAKIPA
NSKAVGINKNDYLQYLDMMKKHVNEEVTEFLKFLQNSAKKCAQDYNMLSDDARLFTEKILR
ACIEQVKKYSEFYTLHEVTSLMGFFPFRVEMGLKLEKTLALGSKYVKTVPFSPMPIKLQ
LSKDDIATITETSEQTAEAMHYDISKDPNAEKLVSRYHPQIALTSQSLFTLLNNHGPTYKE
QWEIPVCIQVIPVAGSKPVKVIYINSPLPQKKMTMRERNQIFHEVPLKFMMSKNTSVPVS
AVFMDKPEEFISEMDMSCEVNECRKIESLENLYLDFDDDVTELETFGVTTTKVSKSPSPA
STSTVPNMTDAPTAPKAGTTTVAPSAPDISANSRSLSQLMEQLQKEKQLVTGMDGGPEE
CKNKDDQGFESCEKVSNSDKPLIQDSLKTS DALQLENSQEIETS NKNDMTIDILHADGE
RPNVLENLDNSKEKTVGSEA AKTEDTVLCSSDTDEECLIIDTECKKTSYNSV
```

**Important features of the protein:****N-glycosylation sites:**

Amino acids 56-60;354-358;427-431

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 187-191;331-335;585-589

**N-myristoylation sites:**

Amino acids 126-132;407-413;557-563

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**FIGURE 63**

TTTTTAACTTGAACCTCCAAGGCCACGTGCGTCTCCTGGCTCCTGCACGGACTGTGTGACTG  
TCCCCGACAGCTTTCTGTCTCGTCTCATGAGGGGTCCAGCACATGGCATTCTGGGTTCGGCA  
CCTGAAGTCCACCTCTATGAGACCCTCTGGGAGCGTGACGGGGCCTTGGCATGGGTTCGGCCG  
AGGCCCTTCTGTCCAGGTCACTGGTGTGGTTCGGCCCAGGCCCTCCTGTCCACATCACCTG  
TGTGGTTCGGCCCAGGCCCTCCTGTCCAGGTACCGGTGTGGTTCGGCCCAGGCCCTCCTGTC  
CAGGTCTCCTGTCCAGGTCACTGGTGTGGTTCGGCCCAGGCCCTTCTGTCCAGGTACCTG  
TGTGGTTCGGCCCAGGCCCTCCTGTACCATGTCACTGTTGAGGGGCTGGCTCTGGAAGAGGG  
CAGGGACTTGGCATTGGTGGGGGCAGGGTTCCAAGGTGTGGCCTGTCAGCAGGAAGGGGCAG  
GTGGCATGGGTCCAGGCGGGACTCAGGGCTGGGGTGCCACTGCTGGAGACTGTCCGGAGGCC  
CCTCCAGGGCACCTTGCCATTGCCATTGTCGCTCATGGCCATCTGGTCCCGTTTCAGGGAAAC  
AAGAGGAGGATCAGATGCTGCGGGACATGATTGAGAAGCTGGGTGACTGGGCCGGGGATGCT  
GAGGGCTGGGCTGGCTGGCTGGGTGGGCCGGGGATGCTGAGTGCTGGGCTGGCTGGCTGGGT  
GGACCGGGCCTCCAGCTGGGGGTGGGGGGGGGGCGGGTATCGGGTCCCCCCTCAGCCTTGG  
TGACAGGACAGGCAGGTTCAACCCTGAGGGTGAGAGCTCCCTCCCGCCCCCTAAGAGAGCCAGG  
GGCAGCTGGTGACCGTGTGGTTCATGGTGGGGACCAGCCCTCCGGGGCACCCAGTCGGGGCAG  
GTTCTCACGTGGGAGGGCACAGGGCTTCCTGCAGGCTCGGAGGCCAGGGCGGATTGTGGCC  
AGTGGAAAGGAAGGATGTTTCTGGCAGGGGGACTTGTGTGGGCCACGGCTGTGCGGCTGCGG  
CGTTGAGCACGGCCTCACTGTCCACCTGTCCCTTAGGCCTCCAGAGGAAGAAGTCCAAGTTC  
CGCTTGTCCTAAGATCTGGTCACCAAAAAGCAAAAGCAGCCCCCTCCAGTAGTAGCCAGTAGG  
GCCGTGGGCTCGGCCCGGACCTGGCATCCGGACTTGGACTCGGGGCCATGGGCTTGGCCCGG  
ACCCGGAACCCGACTTGTACTCGGGGCCGTGGGCTCGGCCCGGACCCGGCATTTCGGACTTG  
GACTCGGGAAGGGCCTCCTGTCCCTACAAGGGGCATGTGGACAGCAGGGACCTGCGCTACCG  
TCTGTGGTCTCAATAAAGAAACCGACCACATGGCCCCGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAACA

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**FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139602
><subunit 1 of 1, 159 aa, 1 stop
><MW: 15900, pI: 8.07, NX(S/T): 0
MGRPRPFCPRSLVWSAQALLSHITCVVGPVPGHRCGRPRPSCPGPPVQVTGVVGP
SVPGHL CGRPRALLYHVTVEGLALEEGRDLALVGAGFQGVACQ QEGAGGMGP
GGTQGWGA
TAGDCPEAPPGHLAIAIVAHGHLVPFQGRGGSDAAGHD
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-25

**N-myristoylation sites:**

Amino acids 109-115;113-119;119-125;148-154;151-157;152-158



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**FIGURE 65**

GGCGACCACCGCCGCCTCCTCACCTGGCCATTGGTGCAGCCCGTTCCCGGCGGGCGAGAGAAG  
GCAGGCGCGCTCCTTGCGCCACGCCACACCGTCGGGGCCCCCGTCGGGTCCCCCTCGGGCCGCA  
**ATGGTGGGCTCCGCGCGGCTGGGTCCGGCACTCTTGACCCCTTTGTAACCACCGCGGCGGG**  
CAGCCAGGGAGTTCGAGCAACGAAGTTGGTGACCTGCCCCGCTCCAGGCAGTTTGCTGTTG  
GGGCTTTCACGGCTGCTGGAAGGGCATGGCTGTTTGTCCCATCACTGGGCGCCAGCTTCTCA  
AAGCTACGTTACAGCAACGCAGTAGGGACTTTCGTGGCAGGCTTTTTTTAAGAGCTGAAAG  
AAGGGCGGGAGGGTTTACGTCC**TAG**GGTGATGATTTCTCACCAGACAGCGAAGTATCTATT  
GGGAACTCCAGGTGACCGCACCTCCTTCGACAGTTCCGCCCCGGGCAAGTTTACCAGCTG  
CGTCAGAAAGCAGGTTTGCAAAATCCTTGAGAACGGCCTGAGCTAAGGACTGGGGTCAGGA  
GGTTTTAACTCATTCTGATTTTCTTGCAATCATATCTCTTGAAAGTTTTTATATTTTCCC  
CAATATTTTTCTGAGTTGCTATATCCAATGAAACAATGCTGATGTAGAGGTCCACCAGCCA  
ATGCTTTATTGGAAGTCAACGAATGAGACCGAGGGTGGCCATAATCAATCTCGGCACGCGG  
GAATGTGAACCTCTTCCAAGGTCTGGGCGAGTCCCTAGAGTTACGCAGATGAAGGACATTGG  
CCCTCGAGAATCTCACACCAGCAAAGAAGAGCACAAACGAAGCGAACTACTTATGATCATT  
GTGGCTTTGGGCAAGTTGTTGTAGCTCCAGCAACAATTTCTTCACCTGGAGTGCAGCAATA  
AATGATACTGGTGTGTCAGGGCAGCTAATAAGCTTCTGAATAATATATGCAAAGTACTTGGC  
ACCATGAGCAGAACTCAGTATACCGTCACTGAAGAAATAGCTTATTTAATGATTACACTTTT  
CATATGTGCAAGTAAAAGTTTGACTTTTAGGGAGAGCCTCACCTACGGAATGTCTTTTTTAA  
ATTTCTTTTTTAATTATACTTTAAGTTCTGGGATACATGTGCAGAACGTGCAGGTTTGTTAC  
ACAGGTATACATGTGCCATGGTGGTTTGCAGCACCCATCAACCCTTCATCTAGGTTTTAAGC  
TCCGCATGCATTAGTTATTTGTCCTAATGCTCTCCCTCCCCTTGTCCCCCACCCECAACAG  
GCCTCAGGGTGTGATGTTCCCCTCCCTGGGTCCATATGTTCTCATTGTTCAACTCCCACTTA  
TGATGAGAACATGCAGTGTTTGGTTTTCTGTTTCTGTGTTAGTTTGCTGAGAATGATGGTTT  
CCAGCATCATCCACGTCCCTGCAAAGGACATGAATTCATTCTTTTTTATGGCTGCATGGTAT  
TCCATGGTGTATATGTGCCACATTTTCTTCATCCAGTCTATCATTGATGGGCACTTGGGTG  
GTTCCAAGACTTTGTTATTGTGAACAGTGCTGCAATAAACATACGTTTGTATGTGTCAAAAA  
AAAAAAAAAAAAAAAA

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**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139632  
><subunit 1 of 1, 90 aa, 1 stop  
><MW: 9586, pI: 12.18, NX(S/T): 0  
MVGSARLGPALLTPFVTTAAGTQGVRA TKLVTC PAPRQFAVGAFTAAGRAWLFVPSLGAS  
FSKLRSQQRSDFRGRLFLRAERRAGGFTS

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**N-myristoylation sites:**

Amino acids 24-30;42-48;58-64

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**FIGURE 67**

**CATG**TCTAGACTGGGAGCCCTGGGTGGTGCCCGTGCCGGGCTGGGACTGTTGCTGGGTACCG  
CCGCCGGCCTTGGATTCTGTGCCTCCTTTACAGCCAGCGATGGAAACGGACCCAGCGTCAT  
GGCCGCAGCCAGAGCCTGCCCAACTCCCTGGACTATACGCAGACTTCAGATCCCGGACGCCA  
CGTGATGCTCCTGCGGGCTGTCCCAGGTGGGGCTGGAGATGCCTCAGTGCTGCCAGCCTTC  
CACGGGAAGGACAGGAGAAGGTGCTGGACCGCCTGGACTTTGTGCTGACCAGCCTTGTGGCG  
CTGCGGCGGGAGGTGGAGGAGCTGAGAAGCAGCCTGCGAGGGCTTGCGGGGGAGATTGTTGG  
GGAGGTCCGATGCCACATGGAAGAGAACCAGAGAGTGGCTCGGCGGCGAAGGTTTCCGTTTG  
TCCGGGAGAGGAGTGACTCCACTGGCTCCAGCTCTGTCTACTTCACGGCCTCCTCGGGAGCC  
ACGTTACAGATGCTGAGAGTGAAGGGGGTTACACAACAGCCAATGCGGAGTCTGACAATGA  
GCGGGACTCTGACAAAGAAAGTGAGGACGGGGAAGATGAAGTGAGCTGTGAGACTGTGAAGA  
TGGGGAGAAAGGATTCTCTTGACTTGAGGAAGAGGCAGCTTCAGGTGCCTCCAGTGCCCTG  
GAGGCTGGAGGTTCTCAGGCTTGAGGATGTGCTGCCCTCCTGCAGCAGGCCGACGAGCT  
GCACAGGGGTGATGAGCAAGGCAAGCGGGAGGGCTTCCAGCTGCTGCTCAACAACAAGCTGG  
TGTATGGAAGCCGGCAGGACTTTCTTGCGCCTGGCCCGAGCCTACAGTGACATGTGTGAG  
CTCACTGAGGAGGTGAGCGAGAAGAAGTCATATGCCCTAGATGAAAAGAAGAAGCAGAGGC  
TGCTCTGGAGAAGGGGGATGAGAGTGCTGACTGTACCTGTGGTATGCGGTGCTTTGTGGTC  
AGCTGGCTGAGCATGAGAGCATCCAGAGGCGCATCCAGAGTGGCTTTAGCTTCAAGGAGCAT  
GTGGACAAAGCCATTGCTCTCAGCCAGAAAACCCCATGGCTCACTTTCTTCTTGGCAGGTG  
GTGCTATCAGGTCTCTCACCTGAGCTGGCTAGAAAAAAAACCTGTACAGCCTTGCTTGAAA  
GCCCTCTCAGTGCCACTGTGGAAGATGCCCTCCAGAGCTTCCTAAAGGCTGAAGAACTACAG  
CCAGGATTTTCCAAAGCAGGAAGGGTATATATTTCCAAGTGCTACAGAGAAGTAGGGAAAAA  
CTCTGAAGCTAGATGGTGGATGAAGTTGGCCCTGGAGCTGCCAGATGTCACGAAGGAGGATT  
TGGCTATCCAGAAGGACCTGGAAGAACTGGAAGTCATTTTACGAGACT**TA**ACCACGTTTCACT  
GGCCTTCATGACTTGATGCCACTATTTAAGGTGGGGGGGCGGGGAGGCTTTTTTCTTAGAC  
CTTGCTGAGATCAGGAAACCACACAAATCTGTCTCCTGGGTCTGACTGCTACCCACTACCAC  
TCCCCATTAGTTAATTTATTCTAACCTCTAACCTAATCTAGAATTGGGGCAGTACTCATGGC  
TTCCGTTTCTGTTGTTCTCTCCCTTGAGTAATCTCTTAAAAAAATCAAGATTCACACCTGCC  
CCAGGATTACACATGGGTAGAGCCTGCAAGACCTGAGACCTTCCAATTGCTGGTGAGGTGGA  
TGAATTCAAAGCTATAGGAACAAAGCACATAACTTGTCACTTTAATCTTTTCACTGACTA  
ATAGGACTCAGTACATATAGTCTTAAGATCATACCTTACCTACCAAGGTAAAAAGAGGGGATCA  
GAGTGGCCACAGACATTGCTTCTTATCACCTATCATGTGAATTCTACCTGTATTCTCTGGG  
CTGGACCACTTGATAACTTCCAGTGTCCTGGCAGCTTTTGGAATGACAGCAGTGGTATGGGG  
TTTATGATGCTATAAAACAATGTCTGAAAAGTTGCCTAGAATATATTTTGTACAAACTTGA  
AATAAACCAAATTTGATGTT

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**FIGURE 68**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139686
><subunit 1 of 1, 470 aa, 1 stop
><MW: 52118, pI: 5.06, NX(S/T): 0
MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG
RHVMLLRVPPGGAGDASVLPSPREGQEKVLDRLDFVLTSLVALRREVEELRSSLRGLAG
EIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESEGGYTTAN
AESDNERDSDKESEDEGEDEVSCETVKMGRKDSLDEEEAASGASSALEAGGSSGLEDVLP
LLQQADELHRGDEQKGREGFQLLLNNKLVIYGSRQDFLWRLARAYSDMCELTEEVSSEKSY
ALDGKEEAEEAALEKGDSEADCHLWYAVLCGQLAEHESIQRRIQSGFSFKEHVDKAIALQP
ENPMAHFLGRWCYQVSHLSWLEKKTATALLSPLSATVEDALQSFLKAEELQPGFSKAG
RVYISKCYRELGKNSEARWWMKLALPELDPVTKEDLAIQKDLEEELEVILRD
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-32

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 209-213

**N-myristoylation sites:**Amino acids 5-11;8-14;9-15;15-21;19-25;72-78;164-170;  
174-180;222-228;230-236**Amidation sites:**

Amino acids 207-211;254-258

**Cell attachment sequence:**

Amino acids 250-253

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**FIGURE 69**

CCCACGCGTCCGAAACACTTTTAAACCTGACCAGCTAAATGGATAAAACCTAGCCTGCATAGCT  
TTTAAACTGGGGTCTCATACAGCACAGGAGGCCTACTTGCTTCAAGAACTGAAAATCCAGAG  
GATGAATTGCTTTATCTGGGAATGGCAAAGCCAGCACAAATAAGGAATGCCAGTTTGTATGG  
GGCTACTAGCTCACATGCGGGATCAGAATGGTGTGAATGACAGCCGCACTGTGTATGAAGG  
TGGTGGTGGTTTCCGCACAAGAGACCAAATAAGAAGAAAGCTGAGAGAGGGGGGAAACGTTTTT  
GGATGACAAAGGATGGGTTTCCATTTAATTACGCAGCTGAAAGGCATGAGTGTGGTGTGGT  
GCTACTTCCTACACTGCTGCTTGTATGCTCACGGGTGCTCAGAGAGCTTGCCCAAAGAACT  
GCAGATGTGATGGCAAATTTGTGTACTGTGAGTCTCATGCTTTCGCAGATATCCCTGAGAAC  
ATTTCTGGAGGGTCACAAGGCTTATCATTAAGGTTCAACAGCATTGAGAAGCTCAAATCCAA  
TCAGTTTGCCGGCCTTAACCAGCTTATATGGCTTTATCTTGACCATAATTACATTAGCTCAGTG  
GATGAAGATGCATTTCAAGGGATCCGTAGACTGAAAGAATTAATTCTAAGCTCCAACAAAAT  
TACTTATCTGCACAATAAAACATTTACCCAGTTCCCAATCTCCGCAATCTGGACCTCTCCT  
ACAATAAGCTTCAGACATTGCAATCTGAACAATTTAAAGGCCTTCGGAAACTCATCATTTTG  
CACTTGAGATCTAACTCACTAAAGACTGTGCCCATAGAGTTTTTCAAGACTGTGCGAATCT  
TGATTTTTTGGATTTGGGTTACAATCGTCTTCGAAGCTTGTCCCGAAATGCATTTGCTGGCC  
TCTTGAAGTTAAAGGAGCTCCACCTGGAGCACAAACAGTTTTTCCAAGATCAACTTTGCTCAT  
TTTCCACGTCTCTTCAACCTCCGCTCAATTTACTTACAATGGAACAGGATTGCTCCATTAG  
CCAAGGTTTGACATGGACTTGGAGTTCCTTACACAACCTTGATTTTATCAGGGAATGACATCC  
AAGGAATTGAGCCGGGCACATTTAAATGCCTCCCCAATTTACAAAAATTGAATTTGGATTCC  
AACAAGCTCACCAATATCTCACAGGAACTGTCAATGCGTGGATATCATTAATATCCATCAC  
ATTGTCTGGAATATGTGGGAATGCAGTCGGAGCATTTGTCTTTATTTTATTGGCTTAAGA  
ATTTCAAAGGAAATAAGGAAAGCACCATGATATGTGCGGGACCTAAGCACATCCAGGGTGAA  
AAGGTTAGTGATGCAGTGGAACATATAATATCTGTTCTGAAGTCCAGGTGGTCAACACAGA  
AAGATCACACCTGGTGCCCCAACTCCCCAGAAACCTCTGATTATCCCTAGACCTACCATCT  
TCAAACCTGACGTCACCCAATCCACCTTTGAAACACCAAGCCCTTCCCCAGGGTTTCAGATT  
CCTGGCGCAGAGCAAGAGTATGAGCATGTTTCATTTACAAAATTATTGCCGGGAGTGTGGC  
TCTCTTTCTCTCAGTGGCCATGATCCTCTTGGTGTATGTGTCTTGAAACGCTACCCAG  
CCAGCATGAAACAACCTCCAGCAACACTCTCTTATGAAGAGGCGGCGGAAAAAGGCCAGAGAG  
TCTGAAAGACAAATGAATTTCCCTTTACAGGAGTATTATGTGGACTACAAGCCTACAACTC  
TGAGACCATGGATATATCGGTTAATGGATCTGGGCCCTGCACATATACCATCTCTGGCTCCA  
GGGAATGTGAGATGCCACACCACATGAAGCCCTTGCCATATTACAGCTATGACCAGCCTGTG  
ATCGGGTACTGCCAGGCCACCAGCCACTCCATGTCACCAAGGGCTATGAGACAGTGTCTCC  
AGAGCAGGACGAAAGCCCCGGCCTGGAGCTGGGCCGAGACCACAGCTTCATCGCCACCATCG  
CCAGGTCGGCAGCACCGGCCATCTACCTAGAGAGAATTGCAAACTAACGCTGAAGCCAACTC  
CTACTGGGGAGCTCCATGGGGGGGAGGGAGGGCCTTCATCTTAAAGGAGAATGGGTGTCCA  
CAATCGCGCAATCGAGCAAGCTCATCGTTCCTGTAAAACATTTATGGCATAGGGGAAAAAA  
AAAAAAAAAAAAAA

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**FIGURE 70**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142392
><subunit 1 of 1, 590 aa, 1 stop
><MW: 67217, pI: 9.26, NX(S/T): 4
MGFHLITQLKGMSVVLVLLPTLLLVMLTGAQRACPKNCRCDGKIVYCESHAFADIPENIS
GGSQGLSLRFNSIQKLKSNQFAGLNQLIWLYLDHNYISSVDEDAFQGIRRLKELILSSNK
ITYLHNKTFHPVPNLRNLDLSYNKLOTQSEQFKGLRKLIIHLRSNSLKTVPPIRVFQDC
RNLDFLDLGYNRLRSLSRNAFAGLLKLKELHLEHNQFSKINFHFPRLFNLRSIYLQWNR
IRSISQGLTWTWSSLHNLDLSGNDIQGIEPGTFKCLPNLQKLNLDNKLNTNISQETVNAW
ISLISITLSGNMWECSRSICPLFYWLKNFKGNKESTMICAGPKHIQGEKVSDAVETYNIC
SEVQVVNTERSHLVPQTPQKPLIIPRPTIFKPDVTQSTFETPSPSPGFGQIPGAEQEYEHV
SFHKIIAGSVALFLSVAMILLVIYVSWKRYPASMKQLQQHSLMKRRRKARESERQMNSP
LQEYYVDYKPTNSETMDISVNGSGPCTYTISGSRECEMPHHMKPLPYYSYDQPVIGYCQA
HQPLHVTKGYETVSPEQDESPGLELGRDHSFIATIAARSAAPAIYLERIAN
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 425-443

**N-glycosylation sites:**

Amino acids 58-62;126-130;291-295;501-505

**Tyrosine kinase phosphorylation site:**

Amino acids 136-143

**N-myristoylation sites:**Amino acids 29-35;61-67;247-253;267-273;271-277;331-337;  
502-508;512-518;562-568**Glycosyl hydrolases family:**

Amino acids 310-319

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**FIGURE 71**

TTCCAGTCAGAGTTAAGTTAAAACAGAAAAAGGAAGATGGCAAGAATATTGTTACTTTTCC  
TCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGAATATTTATGGACCGTCTAGCTTCCAAG  
AAGCTCTGTGCAGATGATGAGTGTGTCTATACTATTTCTCTGGCTAGTGCTCAAGAAGATTA  
TAATGCCCCGGACTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAA  
AGCTGGTAAAAGAAAATGGAGCTGGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAG  
GACGAGATGGGAGTCGTGGGTTATTTCCCCAGGAACCTGGTCAAGGAACAGCGTGTGTACCA  
GGAAGCTACCAAGGAAGTTCCCACCACGGATATTGACTTCTTCTGCGAGTAATAAATTAGTT  
AAAAGCTGCAAATAGAAAGAAAACACCAAAAATAAAGAAAAGAGCAAAGTGGCCAAAAAATG  
CATGTCTGTAATTTTGGACTGACGT

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**FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143076
><subunit 1 of 1, 128 aa, 1 stop
><MW: 14332, pI: 4.83, NX(S/T): 0
MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTISLASAQEDYNAPDCRFINV
KKGQQIYVYSKLVKENGAGEFWAGSVYGDQDEMGVVGYPFRNLVKEQRVYQEATKEVPT
TDIDFFCE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-14

**N-myristoylation site:**

Amino acids 84-90



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**FIGURE 73**

CTCAGATTTGCCATGGAGAAATTTTCAGTCTCGGCAATCCTGCTTCTTGTGGCCATCTCTGG  
TACTCTGGCCAAAGACACCACAGTCAAATCTGGATCCAAAAAGGACCCAAAGGACTCTCGAC  
CCAAACTACCCCAGACCCTGTCCAGAGGTTGGGGAGATCAGCTCATCTGGACTCAGACTTAC  
GAAGAAGCCTTATACAAATCCAAGACAAGCAACAGACCCTTGATGGTCATTTCATCACTTGA  
CGAATGCCC GCACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAGGAGATCCAGAAATTG  
GCAGAGCAGTTTGTTCTCCTCAACTTGATCTATGAAACAACCTGACAAGCACCTTTCTCCTGA  
TGGCCAGTACGTCCCCAGAATTGTGTTTGTGGACCCTTCCCTGACGGTGAGGGCAGACATCA  
CCGGAAGATACTCAAACCGTCTCTACGCTTATGAACCTTCTGACACAGCTCTGTTGCACGAC  
AACATGAAGAAAGCTCTCAAGTTGCTGAAGACAGAGTTGTAGAGTCAACTGTACAGTGCCTC  
AGGAGCCGGGAAGGCAGAAGCACTGTGGACCTGCCGATGACATTACAGTTTAATGTTACAAC  
AAATGTATTTTTTAAACACCCACGTGTGGGGAAACAATATTATTATCTACTACAGACACATG  
ATTTTCTAGAAAATAAAGTCTTGTGAGAACTCCAAA

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**FIGURE 74**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143294  
><subunit 1 of 1, 175 aa, 1 stop, 1 unknown  
><MW: 19888.97, pI: 9.08, NX(S/T): 0  
MEKFSVSAILLLVVAISGTLAKDTTVKSGSKKDPKDSRPKLPQTLSRGWGDQLIWTQTYEE  
ALYKSKTSNRPLMVIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLIYETTDKHLSP  
DGQYVPRIVFVDPSLTVRADITGRYSNRLYAYEPSDTALLHDNMKKALKLLKTEL

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-20

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**FIGURE 75**

GCCGGCGCCAGGGCAGGCGGGCGGGCTGGCAGCTGTGGCGCCGAC**ATGG**CTGCGCTGGTGGAG  
CCGCTGGGGCTGGAGCGGGACGTGTCCCGGGCGGTTGAGCTCCTCGAGCGGCTCCAGCGCAG  
CGGGGAGCTGCCGCCGCAGAAGCTGCAGGCCCTCCAGCGAGTTCTGCAGAGCCGCTTCTGCT  
CCGCTATCCGAGAGGTGTATGAGCAGCTTTATGACACGCTGGACATCACCGGCAGCGCCGAG  
ATCCGAGCCCATGCCACAGCCAAGGCCACAGTGGCTGCCTTCACAGCCAGCGAGGGCCACGC  
ACATCCCAGGGTAGTGGAGCTACCCAAGACGGATGAGGGCCTAGGCTTCAACATCATGGGTG  
GCAAAGAGCAAACTCGCCCATCTACATCTCCCGGGTCATCCAGGGGGTGTGGCTGACCGC  
CATGGAGGCCTCAAGCGTGGGGATCAACTGTTGTGGTGAACGGTGTGAGCGTTGAGGGTGA  
GCAGCATGAGAAGGCGGTGGAGCTGCTGAAGGCGGCCAGGGCTCGGTGAAGCTGGTTGTCC  
GTTACACACCGCGAGTGCTGGAGGAGATGGAGGCCCGGTTGAGAGAAGATGCGCTCTGCCCCG  
CGGCGCCAACAGCATCAGAGCTACTCGTCCTTGGAGTCTCGAGGT**TGA**AACACAGATCTGG  
ACGTTACGTGCACTCTCTTCCTGTACAGTATTTATTGTTCTGGCACTTTATTTAAAGATA  
TTTGACCCTCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 76**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143514  
><subunit 1 of 1, 207 aa, 1 stop  
><MW: 22896, pI: 8.93, NX(S/T): 0  
MAALVEPLGLERDVSRAVELLERLQSGELPPQKLQALQRVLQSRFCSAIREVYEQLYDT  
LDITGSAEIRAHATAKATVAAFTASEGHAHPRVVELPKTDEGLGFNIMGGKEQNSPIYIS  
RVIPGGVADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVLEE  
MEARFEKMRSARRRQQHQSYSSLESRG

**Tyrosine kinase phosphorylation site:**  
Amino acids 51-59

**N-myristoylation sites:**  
Amino acids 102-108;133-139

**Cell attachment sequence:**  
Amino acids 136-139

**PDZ domain (Also known as DHR or GLGF):**  
Amino acids 93-174

## FIGURE 77

[illegible]

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**FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144841
><subunit 1 of 1, 208 aa, 1 stop
><MW: 22187, pI: 5.08, NX(S/T): 1
MDSDETGFHSGSLWVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHL
EIREDTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC
SFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGIL
APQPPDVGSSDPLSMVGPSQGRSPSYAS
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-27

**N-myristoylation sites:**

Amino acids 12-18;20-26;23-29;66-72;94-100;107-113;168-174

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 15-26

**HBGF/FGF family proteins:**

Amino acids 57-73;80-131

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### FIGURE 79

[illegible]

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**FIGURE 80****Protein File:**

MW: 73502.97, pI: 9.26

MSSQPAGNQTS PGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLS  
ILVLLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPD  
EDALPFLT LASAPSQDGKTEAPRGAWKILGLFYAALYYP AACATAGHTAAHLLGSTLS  
WAHLGVQVWQRAECPQVPKIYKYSSLASPLLLGLGFLSLWYPVQLVRSFSRRTGAGSK  
GLQSSYSEEYLRNLLCRKKLGSSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKLVLSA  
TLTGTAIYQVALLLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKHHLW  
ALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCW  
MSFSAYQTAFICLGLLVQQIIFFLGTTALAFVLMPVLHGRNLLLF RSLESSWPFWLTLA  
LAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLFPLNVLVGAMVATWRVLLSALYN  
AIHLGQMDLSLLPPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMA  
APQDSL RPGEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALL  
GANGAQP

**Important features of the protein:****Transmembrane domains:**

Amino acids 54-69;102-119;148-166;207-222;301-320;  
364-380;431-451;474-489;512-531

**N-glycosylation site:**

Amino acids 8-12

**N-myristoylation sites:**

Amino acids 50-56;176-182;241-247;317-323;341-347;525-531;  
627-633;631-637;640-646;661-667

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 364-375

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 132-140



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**FIGURE 81**

AAAAAATACAGCAGGTGAAGGAGGTTGGAGAGTAGGGGGTGGAGGGCCACGCAGCACTTGT  
CCTTCACCCTGGAGGGGATCTGTTACATGCCCCAGATTGCTGGTCCCCTAGAAATGTTACTG  
AGGCAGCCTCTGCATTTTTGCAGGGATTGTTTTCTACTGTTTGACATTCACGTAACCTCCTA  
ACGCTGTCTGGGGAAGATGCTACCCCCTGCTCTCCCCGTCTTTCCTGCACTCTCAGCAATGG  
GATGGGCTGACTGATGCCCTGTGGGCTGGAAAGCTGACCACAGTTGCTGCAGACCAGACCCC  
CTCACATAGTGAGTGCTGGGCTGAGGAATCCAGGAGAGCCCGAGGGGGGACACTGAAGGTGT  
ATCGTTGGCCCTGCCAGCTGCAAGTGAAGTCTTCTGATGAATTTAATAGGGAGAAAGAAG  
TATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATC  
AATATCCCATGAGGCTCATAAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAA  
ACGTCTCCAACATGACTTTCAGCAACGGAAAACCTAAGAGTCAAAGGCATTTATTACCGGAAT  
GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCCTAACTCTGCAGGACCTTCAGCT  
ATGGTGTAATTTGAGGTCAGTGGCCAGAGGACAGATCCCGTCTACATTATGAGTGAAGCGGAGA  
GCTACTGCAGGGTTCTGAGCAGAGTCCTAATTTATATTTTAGAAGAATCATCATGGCTCCTA  
GATTAGGAATAAAACGAAGGGGGCCAGGGATGGAAACGATGAGTCCAGTTGGGTTACTGCAA  
AGATCCAGGCCAGAAATCCAGGCACAGTGGCACACACCTGAGTCCCAGATAATTCCACCTAC  
TGGTCCTGCTCTGTGGCCTACTGGTCCGAGTCCAGCCCCGACTGATTTCTGGGCCTGTAATG  
TCTAAAAACGCTCCCTGCTGATGTTTTGCAAGTGACTGTGTTACTTGAAGGCAGTTCCTAGG  
ATAAACTAGTCGCTTTATCATTACAGAATCATTCACTGAGCATCAACTATGTAACCAGCATT  
GGGTGGGTGCCAGAGATCCAAAGCTAAGACACCAAACCTGCTCTCAGGAAACGAGAGGC  
TGAGAA

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**FIGURE 82**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149995
><subunit 1 of 1, 95 aa, 1 stop
><MW: 10704, pI: 10.00, NX(S/T): 2
MAILTSLQLILLIPSLISHEAHKTSLSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD
ICSRHRVTSAGLTLQDLQLWCNLRVARGQIPSTL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-19

**N-glycosylation sites:**

Amino acids 38-42;41-45

**N-myristoylation site:**

Amino acids 89-95

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**FIGURE 83**

AATAGAAGTCCTCAGGACGGAGCAGAGGTGGCCGGCGGGCCCCGGCTGACTGCGCCTCTGCTT  
TCTTTCCATAACCTTTTCTTTTCGGACTCGAATCACGGCTGCTGCGAAGGGTCTAGTTCCGGA  
CACTAGGGTGCCCGAACGCGCTGATGCCCCGAGTGCTCGCAGGGCTTCCCGCTAACC**ATGCT**  
GCCGCCGCCGCGGGCCCGCAGCTGCCTTGGCGCTGCCTGTGCTCCTGCTACTGCTGGTGGTGC  
TGACGCCGCCCGACCGGCGCAAGGCCATCCCCAGGCCAGATTACCTGCGGCGCGGCTGG  
ATGCGGCTGCTAGCGGAGGGCGAGGGCTGCGCTCCCTGCCGGCCAGAAGAGTGCGCCGCGCC  
GCGGGGCTGCCTGGCGGGCAGGGTGCGCGACGCGTGCGGCTGCTGCTGGGAATGCGCCAACC  
TCGAGGGCCAGCTCTGCGACCTGGACCCAGTGCTCACTTCTACGGGCACTGCGGCGAGCAG  
CTTGAGTGCCGGCTGGACACAGGCGGCGACCTGAGCCGCGGAGAGGTGCCGGAACCTCTGTG  
TGCCTGTCGTTTCGACAGAGTCCGCTCTGCGGGTCCGACGGTCACACCTACTCCCAGATCTGCC  
GCCTGCAGGAGGCGGCCCGCGCTCGGCCGATGCCAACCTCACTGTGGCACACCCGGGGCCC  
TGCGAATCGGGGCCCCAGATCGTGTCACATCCATATGACACTTGGAATGTGACAGGGCAGGA  
TGTGATCTTTGGCTGTGAAGTGTTCCTACCCCATGGCCTCCATCGAGTGAGGAAGGATG  
GCTTGACATCCAGCTGCCAGGGGATGACCCCCACATCTCTGTGCAGTTTAGGGGTGGACCC  
CAGAGGTTTGAGGTGACTGGCTGGCTGCAGATCCAGGCTGTGCGTCCCAGTGATGAGGGCAC  
TTACCGCTGCCTTGGCCGCAATGCCCTGGGTCAAGTGGAGGCCCTGCTAGCTTGACAGTGC  
TCACACCTGACCAGCTGAACTCTACAGGCATCCCCAGCTGCGATCACTAAACCTGGTTCCT  
GAGGAGGAGGCTGAGAGTGAAGAGAATGACGATTACTACT**TAGGT**CCAGAGCTCTGGCCCATG  
GGGGTGGGTGAGCGGCTATAGTGTTTCATCCCTGCTCTTGAAAAGACCTGGAAAGGGGAGCAG  
GGTCCCTTCATCGACTGCTTTTCATGCTGTGTCAGTAGGGATGATCATGGGAGGCCTATTTGACT  
CCAAGGTAGCAGTGTGGTAGGATAGAGACAAAAGCTGGAGGAGGGTAGGGAGAGAAGCTGAG  
ACCAGGACCGGTGGGGTACAAAGGGGCCCATGCAGGAGATGCCCTGGCCAGTAGGACCTCCA  
ACAGGTTGTTTCCCAGGCTGGGGTGGGGGCCTGAGCAGACACAGAGGTGCAGGCACCAGGAT  
TCTCCACTTCTTCCAGCCCTGCTGGGCCACAGTTCTAACTGCCCTTCCTCCCAGGCCCTGGT  
TCTTGCTAATTCCTGGTCCCCAACGTTTATCTAGCTTGTTTGCCCTTTCCCCAACTCATCT  
TCCAGAACTTTTCCCTCTCTCCTAAGCCCCAGTTGCACCTACTAACTGCAGTCCCTTTTGCT  
GTCTGCCGTCTTTTGTACAAGAGAGAGAACAGCGGAGCATGACTTAGTTTCAGTGCAGAGAGA  
TTT

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**FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA167678  
><subunit 1 of 1, 304 aa, 1 stop  
><MW: 32945, pI: 4.69, NX(S/T): 3  
MLPPPRPAAALALPVLLLLLVLTTPPPTGARPSGPDYLRRGWMRLLAEGEGCAPCRPEE  
CAAPRGCLAGVRDACCWECANLEGQLCDLDPSTAHFYGHCGEQLECRDLDGGDLRGE  
VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPCESGPQIVSHPYD  
TWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFVETGWLQI  
QAVRPSDEGTYRCLGRNALGQVEAPASLTVLTPDQLNSTGIPQLRSLNLVPEEEAESEEN  
DDYY

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**N-glycosylation sites:**

Amino acids 159-163;183-187;277-281

**Tyrosine kinase phosphorylation site:**

Amino acids 244-252

**N-myristoylation sites:**

Amino acids 52-58;66-72;113-119;249-255

**Kazal-type serine protease inhibitor domain:**

Amino acids 121-168

**Immunoglobulin domain:**

Amino acids 186-255

**Insulin-like growth factor binding proteins:**

Amino acids 53-90

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**FIGURE 85**

CAAAGCGGCGGGCTGTCCGCGGTGCCGGCTGGGGGCGGAGAGGCGGCGGTGGGCTCCCTGGGG  
TGTGTGAGCCCGGTGATGGAGCCGGGCCCCGACAGCCGCGCAGCGGAGGTGTTTCGTTGCCGCC  
GTGGCTGCCGCTGGGGCTGCTGCTGTGGTCGGGGCTGGCCCTGGGCGCGCTCCCCCTTCGGCA  
GCAGTCCGCACAGGGTCTTCCACGACCTCCTGTCGGAGCAGCAGTTGCTGGAGGTGGAGGAC  
TTGTCCCTGTCCCTCCTGCAGGGTGGAGGGCTGGGGCCTCTGTCGCTGCCCCCGGACCTGCC  
GGATCTGGATCCTGAGTGCCGGGAGCTCCTGCTGGACTTCGCCAACAGCAGCGCAGAGCTGA  
CAGGGTGTCTGGTGCAGCAGCGCCCGGCCCGTGCGCCTCTGTCAGACCTGCTACCCCCTCTTC  
CAACAGGTCGTCAGCAAGATGGACAACATCAGCCGAGCCGCGGGGAATACTTCAGAGAGTCAG  
AGTTGTGCCAGAAGTCTCTTAATGGCAGATAGAATGCAAATAGTTGTGATTCTCTCAGAATT  
TTTTAATAACCATGCGCAGGAGGCAAATTGTGCAAATTGTTTAACAAACAACAGTGAAGAAT  
TATCAAACAGCACAGTATATTTCCCTTAATCTATTTAATCACACCCTGACCTGCTTTGAACAT  
AACCTTCAGGGGAATGCACATAGTCTTTTACAGACAAAAAATTATTCAGAAGTATGCAAAAA  
CTGCCGTGAAGCATACAAACTCTGAGTAGTCTGTACAGTGAAATGCAAAAAATGAATGAAC  
TTGAGAATAAGGCTGAACCTGGAACACATTTATGCATTGATGTGGAAGATGCAATGAACATC  
ACTCGAAAACATATGGAGTCGAACCTTTCAACTGTTTCAGTCCCTTGACAGTGACACAGTGCCTGT  
AATTGCTGTTTCTGTGTTTCATTCTCTTTCTACCTGTTGTCTTCTACCTTAGTAGCTTTCTTC  
ACTCAGAGCAAAAGAAACGCAAACCTCATTCTGCCCAAACGTCTCAAGTCCAGTACCAGTTTT  
GCAAATATTCAGGAAAATTCAAACTGAGACCTACAAAATGGAGAATTGACATATCACGTGAA  
TGAATGGTGAAGACACAACCTTGGTTTCAGAAAGAAGATAAACTGTGATTTGACAAGTCAAG  
CTCTTAAGAAATACAAGGACTTCAGATCCATTTTTTAATAAGAATTTTCGATTTTTCTTTCC  
TTTTCCACTTCTTCTAACAGATTTGGATATTTTTTAATTTCCAG

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**FIGURE 86**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA168028
><subunit 1 of 1, 334 aa, 1 stop
><MW: 37257, pI: 5.95, NX(S/T): 10
MEPGPTAAQRRCSLPPWLPLGLLLWSGLALGALPFGSSPHRVFHDLLSEQQLLEVEDLSL
SLLQGGGLGPLSLPPDLPDLDPEDCRELLLDNFANSSAELTGCLVRSARPVRLCQTCYPLFQ
QVVS KMDNISRAAGNTSESQSCARSLLMADRMQIVVILSEFFNTTWQEANCANCLTNNSE
ELSNSTVYFLNLFNHTLTCTFEHNLQNAHSLLOTKNYSEVCKNCREAYKTLSSLYSEMOK
MNELENKAEPGTHLCIDVEDAMNITRKLWSRTFNCSVPCSDTVPVIAVSVFILEFLPVVY
LSSFLHSEQKKRKLILPKRLKSSTSFANIQENSN
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-31

**Transmembrane domain:**

Amino acids 278-300

**N-glycosylation sites:**Amino acids 93-97;128-132;135-139;163-167;177-181;  
184-188;194-198;216-220;263-267;274-278**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 10-14

**N-myristoylation sites:**

Amino acids 27-33;206-212;251-257

**Leucine zipper pattern:**

Amino acids 190-212

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**FIGURE 87**

**ATG**CTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCAGGGC  
GGGCAGGCGCCCCGCGCGGGCCGCGGGGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGC  
TGTACGGGCGCCTGGCGGCCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCG  
CGTGAGCAGGCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCGCGACCGCCGCTTCCG  
GCCGCCACCAACCTGCGCAGCGTGTGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGA  
GGTACCCACAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTC  
GGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCACCGTCGTCTTGCGCCG  
CACCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCAACATCCCCGTGG  
GCTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAA  
CAGGGCGCCAAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCC**TG**AGGCCGGTCTCTG  
CCCCGGGAGGTCTCCCCGGCCCGCATCCCGAGGCGCCCAAGCTGGAGCCGCTTGGAGGGCTC  
GGTCGGCGACCTCTGAAGAGAGTGCACCGAGCAAACCAAGTGCCGGAGCACACGCGCCGCT  
TTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCATCCCTGGCTTGCTTTTAGCTAC  
AAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGGGCATCCTGTGTGCGGC  
CCGCATGGAGGGTTTGGAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATCGGCTGCT  
GCGGGTGCAGGGCGTGACTCACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTT  
TTAAAGCAATCTAAAAATAATAAAGTATAGCGACTATATACCTACTTTTAAATCAACTG  
TTTTGAATAGAGGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTA  
ACATATAAACATCGTTTTTTTACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTT  
GGATAAATTTTGTAGCTGGTACACTCTGGCCTGGGTCTCTGAATTCAGCCTGTCAACGATGG  
CTGACTGATGAAATGGACACGTCTCATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCAG  
GGCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGT  
TCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGCACAATT  
TTTTCCCCCTTTTGAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGT  
GGAACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGG  
GCTTTAGGATCAGGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAAT  
CTGGAGGCTTCTGTTTCTGCATTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATT  
GAAAGTCTGTCTCTGAACACAATTATTTGTAAAAGTTAGTAGTTCTTTTTTAAATCATTAAA  
AGAGGCTTGCTGAAGGAT

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**FIGURE 88**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA173894
><subunit 1 of 1, 202 aa, 1 stop
><MW: 21879, pI: 9.30, NX(S/T): 2
MLVAGFLLALPPSWAAGAPRAGRPPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQL
GPREQARNASCPAGGRPGDRRFRPPTNLRVSPWAYRISYDPARYPRYLPEAYCLCRGCL
TGLFGEEDVRFERSAPVYMPTVVLR RTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSI
NSSIDKQGAKLLLGPNDAPAGP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-15

**N-glycosylation sites:**

Amino acids 68-72;181-185

**Tyrosine kinase phosphorylation site:**

Amino acids 97-106

**N-myristoylation sites:**

Amino acids 17-23;49-55;74-80;118-124

**Amidation site:**

Amino acids 21-25



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**FIGURE 89**

CCGGGGCCTCCGGAGAACGCTGTCCCATGAACGTGCGGGGAGCGGGCCCCGGCGTCCGCGCG  
TCCCCGCGTCCCTGGCAATTCCCGACTTCCCAACGGCTTCCCGCTGGCAGCCCCGAAGCCGC  
ACCATGTTCGCGCTCTGGTTGCTGCTGGCCGGGCTCTGCGGCCTCCTGGCGTCAAGACCCGGT  
TTTCAAAATTCACTTCTACAGATCGTAATTCCAGAGAAAATCCAAACAAATACAAATGACAG  
TTCAGAAATAGAATATGAACAAATATCCTATATTATTCCAATAGATGAGAACTGTACACTG  
TGCACCTTAAACAAAGATATTTTTTTAGCAGATAATTTTATGATCTATTTGTACAATCAAGGA  
TCTATGAATACTTATTCTTCAGATATTTCAGACTCAATGCTACTATCAAGGAAATATTGAAGG  
ATATCCAGATTCCATGGTCACACTCAGCACGTGCTCTGGACTAAGAGGAATACTGCAATTTG  
AAAATGTTTCTTATGGAATTGAGCCTCTGGAATCTGCAGTTGAATTTTCAGCATGTTCTTTAC  
AAATTAAAGAATGAAGACAATGATATTGCAATTTTTATTGACAGAAGCCTGAAAGAACAACC  
AATGGATGACAACATTTTTATAAGTGAAAAATCAGAACCAGCTGTTCCAGATTTATTTCCCTC  
TTTATCTAGAAATGCATATTGTGGTGGACAAAACCTTGTATGATTACTGGGGCTCTGATAGC  
ATGATAGTAACAAATAAAGTCATCGAAATTGTTGGCCTTGCAAATTCATGTTCCACCAATT  
TAAAGTTACTATTGTGCTGTCATCATTTGGAGTTATGGTTCAGATGAAAATAAGATTTCTACAG  
TTGGTGAGGCAGATGAATTATTGCAAAAATTTTTAGAAATGGAACAATCTTATCTTAACCTA  
AGGCCTCATGATATTGCATATCTACTAATTTATATGGATTATCCTCGTTATTTGGGAGCAGT  
GTTTCCTGGAACAATGTGTATTACTCGTTATTTCTGCAGGAGTTGCATTGTACCCCAAGGAGA  
TAACTCTGGAGGCATTTGCAGTTATTGTACCCAGATGCTGGCACTCAGTCTGGGAATATCA  
TATGACGACCCAAAGAAATGTCAATGTTTCAGAAATCCACCTGTATAATGAATCCAGAAGTTGT  
GCAATCCAATGGTGTGAAGACTTTTAGCAGTTGCAGTTTGAGGAGCTTTCAAAATTTTCAATTT  
CAAATGTGGGTGTCAAATGTCTTCAGAAATAAGCCACAAATGCAAAAAAATCTCCGAAACCA  
GTCTGTGGCAATGGCAGATTGGAGGGAAATGAAATCTGTGATTGTGGTACTGAGGCTCAATG  
TGGACCTGCAAGCTGTTGTGATTTTCGAACCTTGTGTACTGAAAGACGGAGCAAAATGTTATA  
AAGGACTGTGCTGCAAGACTGTCAAATTTTACAATCAGGCGTTGAATGTAGGCCGAAAGCA  
CATCCTGAATGTGACATCGCTGAAAATTTGTAATGGAAGCTCACCAGAATGTGGTCTTGACAT  
AACTTTAATCAATGGACTTTTCATGCAAAAATAATAAGTTTATTTGTTATGACGGAGACTGCC  
ATGATCTCGATGCACGTTGTGAGAGTGTATTTGGAAAAGGTTCAAGAAATGCTCCATTTGCC  
TGCTATGAAGAAATACAATCTCAATCAGACAGATTTGGGAACCTGTGGTAGGGATAGAAATAA  
CAAATATGTGTTCTGTGGATGGAGGAATCTTATATGTGGAAGATTAGTTTGTACCTACCCTA  
CTCGAAAGCCTTTCCATCAAGAAAATGGTGATGTGATTTATGCTTTTCGTACGAGATTCTGTA  
TGCATAACTGTAGACTACAAATTGCCTCGAACAGTTCCAGATCCACTGGCTGTCAAAAATGG  
CTCTCAGTGTGATATTGGGAGGGTTTGTGTAAATCGTGAATGTGTAGAATCAAGGATAATTAAG  
GCTTCAGCACATGTTTGTTCACAACAGTGTCTGGACATGGAGTGTGTGATTCCAGAAACAA  
GTGCCATTGTTTCGCCAGGCTATAAGCCTCCAAACTGCCAAATACGTTCCAAAGGATTTTCCA  
TATTTCTGAGGAAGATATGGGTTCAATCATGGAAAGAGCATCTGGGAAGACTGAAAACACC  
TGGCTTCTAGGTTTTCCTCATTTGCTCTTCCTATTCTCATTGTAACAACCGCAATAGTTTGGC  
AAGGAAACAGTTGAAAAAGTGGTTCGCCAAGGAAGAGGAATCCCAAGTAGCGAATCTAAAT  
CGGAAGGTAGCACACAGACATATGCCAGCCAATCCAGCTCAGAAGGCAGCACTCAGACATAT  
GCCAGCCAAACCAGATCAGAAAGCAGCAGTCAAGCTGATACTAGCAAATCCAAATCAGAAGA  
TAGTGCTGAAGCATATACTAGCAGATCCAAATCACAGGACAGTACCCAAACACAAAGCAGTA  
GTAACTAGTGATTCCCTTCAGAAGGCAACGGATAACATCGAGAGTCTCGCTAAGAAATGAAAA  
TTCTGTCTTTCCTTCCGTGGTCACAGCTGAAAGAAACAATAAATTGAGTGTGGATC

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**FIGURE 90**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA176775
><subunit 1 of 1, 787 aa, 1 stop
><MW: 87934, pI: 5.49, NX(S/T): 4
MFRLWLLLAGLCGLLASRPGFQNSLLQIVIPEKIQTNTNDSSEIEYEQISYIIPIDEKLY
TVHLKQRYFLADNFMIIYLYNQGSMTYSSDIQTQCYQGNIEGYPDMSVTLSTCSGLRGI
LQFENVSYGIEPLESAVEFQHVLYKLKNEEDNDIAIFIDRSLKEQPMDDNIFISEKSEPAV
PDLFFPLYLEMHIVVDKTLTYDYGSDSMIVTNKVIEIVGLANSMTQFKVTIVLSSLELWS
DENKISTVGEADELLQKFLEWKQSYLNLRPHDIAYLLIYMDYPRYLGAFFPGTMCITRYS
AGVALYPKEITLEAFQAVIVTQMLALSGLISYDDPKKCQCSESTCIMNPEVVQSNQVKTFS
SCSLRSFQNFISNVGVKCLQNKPMQKSPKPVCGNGRLEGNEICDCGTEAQC GPASCCD
FRTCVLKDGAICYKGLCKDCQILQSGVECRPKAHPECDIAENCNGSSPEC GPDITLING
LSCKNKFKICYDGDCHDLARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGRDRNNKYV
FCGWRNLICGRLVCTYPTRKPFHQENGDVIIYAFVRDSVCITVDYKLPRTVPDPLAVKNGS
QCDIGRVCVNRECYESRIIKASAHVCSQCSGHGVCDNRNKCHCSPGYKPPNCQIRSKGF
SIFPEEDMGSIMERASGKTENTWLLGFLIALPILIVTTAIVLARKQLKKWFAKEEEFPSS
ESKSEGSTQTYASQSSSEGSTQTYASQTRSESSSQADTSKSKSEDSAEAYTSRSKSDST
QTQSSSN

```

**Important features of the protein:****Signal peptide:**

Amino acids 1-16

**Transmembrane domain:**

Amino acids 309-326; 681-705

**N-glycosylation sites:**

Amino acids 39-43; 125-129; 465-469; 598-602

**Glycosaminoglycan attachment site:**

Amino acids 631-635

**Tyrosine kinase phosphorylation site:**

Amino acids 269-276

**N-myristoylation sites:**Amino acids 13-19; 82-88; 99-105; 218-224; 401-407; 634-640;  
726-732; 739-745**EGF-like domain proteins:**

Amino acids 642-654

**Disintegrins proteins:**

Amino acids 400-407; 422-472; 403-453; 467-517; 634-684

**Reprolysin (M12B) family zinc metalloprotease:**

Amino acids 186-383

**Reprolysin family propeptide:**

Amino acids 63-176

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**FIGURE 91**

CACCAGACAGCACTCCAGCACTCTGTTTGGGGGGCATTGAAACAGCAAAATCACTCATATAA  
AGGCAAAAATTTGCAAAAAAATAGTAATAACCAGCATGGCACTAAATAGACCATGAAAAG  
ACATGTGTGTGCAGTATGAAAATTGAGACAGGAAGGCAGAGTGTGAGCTTGTTCACCTCAG  
CTGGGAATGTGCATCAGGCAACTCAAGTTTTTACCACGGCATGTGTCTGTGAATGTCCGCA  
AAACATTCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTGTGG  
ATGCTCCCTTCACTCTGCAAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAACATTTC  
CTGTGTCTACTACTATAGGAAAAATTTAACCTGCACCTGGAGTCCAGGAAAGGAAACCAGTT  
ATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACAACC  
AATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTTCCTTCCAAGAATAACGATCCC  
AGATAATTATACCATTTGAGGTGGAAGCTGAAAATGGAGATGGTGTAAATTAATCTCATATGA  
CATACTGGAGATTAGAGAACATAGCGAAAACCTGAACCACCTAAGATTTTCCGTGTGAAACCA  
GTTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAAGCCTGAGTTGGCGCCTGTTTC  
ATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGTACCAGCTGGATGGAAGTCA  
ACTTCGCTAAGAACCGTAAGGATAAAAACCAACGTACAACCTCACGGGGCTGCAGCCTTTT  
ACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAGTCAAAGTTCTGGAGTGACTGGAG  
CCAAGAAAAAATGGGAATGACTGAGGAAGAAGCTCCATGTGGCCTGGAAGTGTGGAGAGTCC  
TGAAACCAGCTGAGGCGGATGGAAGAAGGCCAGTGCCTGTTGTTATGGAAGAAGGCAAGAGGA  
GCCCCAGTCCTAGAGAAAAACACTTGGCTACAACATATGGTACTATCCAGAAAGCAACACTAA  
CCTCACAGAAACAATGAACACTACTAACACAGCAGCTTGAAGTGCATCTGGGAGGCGAGAGCT  
TTTGGGTGTCTATGATTTCTTATAATTCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATT  
CCAGCTATTCAAGAAAAATCATTTTCAGTGCATTGAGGTGATGCAGGCCTGCGTTGCTGAGGA  
CCAGCTAGTGGTGAAGTGGCAAAGCTCTGCTCTAGACGTGAACACTTGGATGATTGAATGGT  
TTCCGGATGTGGACTCAGAGCCCCACCACCTTTTCCCTGGGAATCTGTGTCTCAGGCCACGAAC  
TGGACGATCCAGCAAGATAAATTAACCTTTCTGGTGCTATAACATCTCTGTGTATCCAAT  
GTTGCATGACAAAGTTGGCGAGCCATATCCATCCAGGCTTATGCCAAAGAAGGCGTTCCAT  
CAGAAGGTCCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAA  
GAGATTCCCAAGAGTGAGAGAAAGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGA  
AGGTGGAAAAGGATTCTGTAAGCACGCCCATAGCGAAGTGGAAAAAACCCTAAGCCCCAGA  
TAGATGCTATGGATAGACCTGTTGTAGGCATGGCTCCCCATCTCATTTGTGACTTGCAACCT  
GGCATGAATCACTTAGCTTCTTTAAATCTCTCTGAAAATGGGGCCAAGAGCACCCACCTTTT  
GGGGTTTTGGGGTTAAATGAGAGTGAAGTGACAGTACCTGAGAGGAGAGTCCCTGAGGAAAT  
GGAAGGAGTTGTTATTAATTTTGTCTGTTAGGCCCTGAATTGACCTCCCGGAGCTCCCCGA  
CCATCATTCCCAGGAATGGCGTGCCTGGCTTAAAGAGTGAGGAGGAACAGACCCTGTACCA  
TGACTTCTACTGCCCCTGCCAAATCATGCTTTTGTGTTTTTTCAGTCCACCTTATCTCCTGACATCT  
TAAATACTGGGCAAGGCTTGGATTCTTGCTTAGGCTAAATAATTTTTTCTTATGGTAAAATA  
CACGTAAAATATTTTTCCAGTTTAAACATTTGAAAGTGTACAATTTAGTGGCATTAGAAGCA  
TTCACAATATTGTGCAACCATCACCACTATTTCCAGAACTCTTCTATTTCTGCCCAAATAGA  
AGCCCTATACCCATTTCATTAGTCACTCCCCATTTCCTCTCCTCCCACAGCCCCTGGCAACTAC  
CAAACGTCTTTGTGTCTCTATGGATTGCCTATTTTGGATATTTTCATATACATAGAATCATAA  
ANTAAAAA

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**FIGURE 92**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA177313
><subunit 1 of 1, 582 aa, 1 stop
><MW: 66605, pI: 8.14, NX(S/T): 15
MCIRQLKFFTTACVCECPQNILSPQPSVNLGMMWTWALWMLPSLCKFSLAALPAKPENI
SCVYYRKNLTCTWSPGKETSQYTVKRTYAFGEKHDNCTTNSSTSENRASCSFFLPRI
TIPDNYTIEVEAENG DGVKSHMTYWRLENI AKTEPPKIFRVKPV LGIKRMIQIEWIKPE
LAPVSSDLKYTLRFRTVNSTSWMEVNF AKNRKDKNQTYNLTGLQPFTEYVIALRCAVKES
KFWS DWSQEKMGMT EEEAPCGLELWRVLKPAEADGR RPVRL L WKKARGAPVLEKTLGYNI
WYYPESNTNLTETMNTTNQQLHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQC
IEVMQACVAEDQLVVKWQSSALDVNTWMIEWFPD VDSEPTT LSWESVSQATNWTIQQDKL
KPFWCYNISVYPMLHDKVGEPYSIQAYAKEGVPSEGPETKVENIGVKT V TITWKEIPKSE
RKGII CNYTIFYQAEGGKGFC KHAHSEVEKNPKPQIDAMDRPVVGMAPP SHCDLQPGMNH
LASLNLS ENGA KSTHLLGFWGLNESEVTV PERRVLRKWKELL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-46

**N-glycosylation sites:**Amino acids 59-63;69-73;99-103;103-107;125-129;198-202;  
215-219;219-223;309-313;315-319;412-416;  
427-431;487-491;545-549;563-567**N-myristoylation sites:**

Amino acids 32-38;137-143;483-489;550-556;561-567

**Amidation site:**

Amino acids 274-278

**Growth factor and cytokines receptors family signature 1:**

Amino acids 62-75

**Fibronectin type III domain:**

Amino acids 54-144;154-247

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**FIGURE 93**

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT  
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA  
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCAGCTGGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG  
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

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**FIGURE 94**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57700

&lt;subunit 1 of 1, 125 aa, 1 stop

&lt;MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSLWLCQPTPRCGNKIYNPSEQCCYDDAI

LSLKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPIRSCTRNRR

HVLYP

**Important features:****Signal peptide:**

Amino acids 1-21

**N-myristoylation sites:**

Amino acids 33-39;70-76

**Anaphylatoxin domain proteins:**

Amino acids 50-60

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**FIGURE 95**

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT  
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT  
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT  
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACCTATTCATGCTTCCTGTGATTTC  
ATCCAACCTACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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**FIGURE 96**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62872  
<subunit 1 of 1, 90 aa, 1 stop  
<MW: 9039, pI: 4.37, NX(S/T): 1  
MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTT  
ATTAASTTARKDIPVL PKWVGDL PNGRVCP

**Important features:****Signal peptide:**

Amino acids 1-19



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**FIGURE 97**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG  
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACCAACAGGCTGG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAACTGAGAAAT  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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**FIGURE 98**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62876  
<subunit 1 of 1, 120 aa, 1 stop  
<MW: 12925, pI: 9.46, NX(S/T): 0  
MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGR  
AGGGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

**Important features:****Signal peptide:**

Amino acids 1-17

**N-myristoylation sites:**

Amino acids 58-64;63-69;64-70;83-89;111-117;115-121

### FIGURE 99

[illegible]

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**FIGURE 100**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66660
><subunit 1 of 1, 209 aa, 1 stop
><MW: 21588, pI: 5.50, NX(S/T): 0
MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQML
TLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEELP
QIFTSLLIHS LFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSGTDD
DFAVTTPAGIQRSTHAIEEATTESANGIQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-16

**Leucine zipper patterns:**

Amino acids 10-32;17-39

**N-myristoylation sites:**Amino acids 12-18;25-31;36-42;74-80;108-114;111-117;  
135-141;151-157;159-165;166-172;189-195

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**FIGURE 101**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCGAGCTATTAGAGGTCCACCCCAAACCTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTGAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTTATACAATG

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**FIGURE 102**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGARSPLKPLPLEEQV  
EWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQOMFALGERLRKNYVEDIP  
FLSPTFNPQEVFIRTNIFRNLESTRCLLAGLFQCQKEGP IIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTA  
SLQPGISED LKKVKDRMGIDSSDKVDFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRES  
LQMAVGPFLLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESK  
EWFVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

**Important features:**

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

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**FIGURE 103**

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGA  
CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCGCCTC  
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT  
GGGGCCTGGGGTGCAGGGCTGCCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT  
GCACTGCCCCGCCAGGGGACCACGGTGGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC  
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA  
GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCCTGCTGCTGCTGG  
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG  
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG  
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCC  
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC  
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC  
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGCCCCCTGGGTGCGCGAGAGCCACGTCACA  
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT  
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACACAGCCACAGTGCCACCA  
CGAGGCCCGTGGTGCGGGAGCCCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC  
CCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC  
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG  
GGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGC  
CAGATGGGGCAGGGGACACGGGCCAGCCCTACACCAGTACGCGCGAGGCCACCACGGTCCCT  
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC  
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT  
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTGCTGCTGAGTACACGGTCAACCAGCTGCG  
GCCAACGCCACTTACTCCGTCTGTGTGTCATGCCCTTGGGGCCCGGGCGGGTGCCGGAGGGCG  
AGGAGGCCTGCGGGGAGGCCATACACCCCGAGCCGTCCACTCCAACCAGCCCCAGTCACC  
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTTGCGCCCGCCCTGGCCGCGGTGCTCCTGGC  
CGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG  
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTC  
CCCTTGAGGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA  
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTACCCCTCCACGCAAAGC  
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA  
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCAGTGCCTATGAGGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG  
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG  
AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA  
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAATC  
AGAGACAAGGACTTTGGTTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAA  
ATAAAAAAAAAA

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**FIGURE 104**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

&lt;subunit 1 of 1, 598 aa, 1 stop

&lt;MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLL LLL LLL LLL ALGPGVQGCPSGCQCSQPQT V FCTARQGT TVPRDVPPDTVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLR LPR LLL LLDLSHNSLLALEPGILDTANVEALRL  
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSLQALPGDLSGLFPRLRL LAAARNPFNCVCPLSWFGPWVRESHVTLASP  
EETRCHFP PKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSP PPTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQ  
GTRPSPTPVTPRPPRSLTLGIEPVSP TSLRVGLQRYLQGS SVQLRSLRLTYRNLSGPDKRLV  
TLRLPASLA EYTVTQLRP NATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVR RGRAMAAAAQDKGQVGP GAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFP GPGLQSPLHAKPYI

**Signal sequence.**

amino acids 1-23

**Transmembrane domain.**

amino acids 501-522

**N-glycosylation sites.**

amino acids 198-202, 425-429, 453-457

**Tyrosine kinase phosphorylation site.**

amino acids 262-270

**N-myristoylation sites.**

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**EGF-like domain cysteine pattern signature.**

amino acids 355-367

**Leucine zipper pattern.**

amino acids 122-144, 194-216



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**FIGURE 105**

CCCACGCGTCCGAAGGCAGACAAAGGTTTCATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCCAAACCTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTCAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTTCG  
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCCCTGATTTC  
CCACAAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAAA

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**FIGURE 106**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758  
<subunit 1 of 1, 98 aa, 1 stop  
<MW: 11081, pI: 6.68, NX(S/T): 1  
MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDNHCHNLPEGVADLTQIDVNVQDHF  
W  
DGKGCEMICYC�FSELLCCPKDVFFGPKISFVIPCNQ

**Important features:****Signal peptide:**

Amino acids 1-20

**N-glycosylation site:**

Amino acids 72-76

**Tyrosine kinase phosphorylation site:**

Amino acids 63-71

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**FIGURE 107**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTCACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCCTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTTCCTCGGCCC  
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTA  
TCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCT  
TTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTA  
ACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCAT  
AGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTC  
CTACATTAAAAATATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAAA  
AA

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## **FIGURE 108**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59849
<subunit 1 of 1, 135 aa, 1 stop
<MW: 14833, pI: 9.78, NX(S/T): 0
MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGL
LKALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLG
STGKSSLGTEEQRPL
```

**Important features:**

**Signal peptide:**

Amino acids 1-18

**Tyrosine kinase phosphorylation site:**

Amino acids 36-45

**N-myristoylation sites:**

Amino acids 33-39;59-65

**Amidation site:**

Amino acids 90-94

**Leucine zipper pattern:**

Amino acids 43-65

**Tachykinin family signature:**

Amino acids 86-92

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**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCC**TGA**  
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTGTGTTT  
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGGAATCC  
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCCC  
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAAGTGAGGCCTG  
GGGTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM  
MFEGKANESSPKPVGPPPERDIASLP

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**FIGURE 111**

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA  
AAGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA  
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAG  
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCAC  
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT  
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG  
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCTGTTAATAAAAGAAA  
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA  
ATAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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**FIGURE 112**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290  
><subunit 1 of 1, 85 aa, 1 stop  
><MW: 9700, pI: 9.55, NX(S/T): 0  
MKKVLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPR  
FPWFRRNFPIPIPIESAPTTPLPSEK

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**Homologous region to B3-hordein:**

Amino acids 47-85



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**FIGURE 113**

CTCCTCTTAACATACTTGCAGCTAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCA**ATGG**CTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA  
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGTATAACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTGCG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGT**AG**GTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACCTACATCA  
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAGATAGCAC  
TATGTGTTCAAA

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**FIGURE 114**

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**  
amino acids 1-15

**Casein kinase II phosphorylation site.**  
amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**  
amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**  
amino acids 196-200

**Speract receptor repeated domain signature.**  
amino acids 29-67, 249-287

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**FIGURE 115**

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGAT  
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG  
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT  
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT  
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG  
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT  
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT  
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG  
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCAGTCAGAGCTATAA  
GAGATGATGGAAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA  
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAAATATTACTATTTAGTTTTTTTA  
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAATCTGA

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**FIGURE 116**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896  
<subunit 1 of 1, 166 aa, 1 stop  
<MW: 19171, pI: 8.26, NX(S/T): 1  
MMLHSALGLCLLLVTVSSNLAIAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQKSKK  
PLMVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIM  
FVDPSLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

**Important features:****Signal peptide:**

Amino acids 1-23

**N-myristoylation site:**

Amino acids 51-57

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**FIGURE 117**

CCTGGAGCCGGAAGCGGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA  
GCCTAGCGTGTCCACGATGCGGGCTGGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATCG  
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCC  
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCTCGGCTGGAGCCAGTTCTAACTG  
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG  
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAA  
AAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT  
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTC  
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTT  
TATGGAGATGAAACCTGGGTAAATTATTCCTCAAAGCATTTTGTGGAATATGATGGAACAAC  
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG  
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC  
CACATTTTCAGGGCCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT  
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCCTTACCCAATTTGCTGG  
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG  
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA  
TCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA  
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG  
CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC  
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAAATGTCAGAAAGATTGCATGGGAACT  
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGTT  
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA  
GTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTC  
CCACTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTCGGCCGT  
TCACGTCATTGTGTGCACCTCAGCTGAAAGTTCTGTGCTACTTCTGTGGCCTCTCGTGGCTGG  
CGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGGC  
AGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGT  
GTCCCGACACAGGTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTCACAGAGGAACAAGCCCC  
CCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAG  
GGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACT  
CATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGAC  
GTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTCTGTTAGCTGGGGAGTGG  
TGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCAGGATCAAGG  
GACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATCC  
CCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTTT  
GTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGCC  
CATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTAG  
TTACCAAAAAGAATAAACGGCAATAATTGAGAAAAAAA

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**FIGURE 118**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920
><subunit 1 of 1, 310 aa, 1 stop
><MW: 33875, pI: 7.08, NX(S/T): 2
MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL
PPPLFSKVIVILIDALRDDFVFGSKGVKEMPYTTYLVEKGASHSFVAEAKPPTVTMPRIK
ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGT
TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMD
SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP
GDIRHPKHVQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-34

**Transmembrane domain:**

Amino acids 58-76

**N-glycosylation sites:**

Amino acids 56-60;194-198

**N-myristoylation sites:**Amino acids 6-12;52-58;100-106;125-131;233-239;270-276;  
275-281;278-284**Amidation site:**

Amino acids 154-158

**Cell attachment sequence:**

Amino acids 205-208

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**FIGURE 119**

GCCACGCGTCCG**ATG**GCGTTACGTTGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTGCGCACATTATAGCATTTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCTGAATCCCCTTGTAAGTACCTCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGTCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGG  
TGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTTT  
GGTGAGCTCT**TAGA**ACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACC  
AAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTT  
ACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTGT  
TTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATG  
ATTACCTCTGGTGTGACAGGTTTGAACCTGCACTTCTTAAGGAACAGCCATAATCCTCTGA  
ATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTATAGGAACTTGTAG  
GGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGCT  
TCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCCTCATCTGTCA  
TGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTCCCTTCGCTTG  
AATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAAT  
ATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTTG  
TGAAGAATGCATTTAAAGCTATTTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAGA  
AATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGT  
ACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGTG  
CAATACAATAAACTCTGAAATTAAGACTC

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**FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330  
<subunit 1 of 1, 144 aa, 1 stop  
<MW: 16699, pI: 5.60, NX(S/T): 0  
MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA  
FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW  
CKLAFYLLAFFYYLYGMIYVLVSS

**Important features:****Signal peptide:**

Amino acids 1-20

**Type II transmembrane domain:**

Amino acids 11-31

**Other transmembrane domain:**

Amino acids 57-77;123-143

**Glycosaminoglycan attachment site:**

Amino acids 96-100



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**FIGURE 121**

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTTCGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG  
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTGGAG  
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTTGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTTACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT  
TCTGTGTTACACATCCCCACCCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA  
AAGGTCTTGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 122**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG  
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGP EESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG  
IIICALATLAAKGDLVFTAI FIGAVAAMTGYWLSERSDRVLEGF I KGR

**Important features:****Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 342-392

**N-glycosylation sites:**

Amino acids 79-83;205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 290-294

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 321-333

**EGF-like domain cysteine pattern signature:**

Amino acids 181-193

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**FIGURE 123**

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCC  
TCTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCAC  
AACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCA  
CCCCCTGGCCACACTCTTCAAGATCCTGGCGTCCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCA  
TGTACACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGC  
TACAGCGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTA  
CTCCAAGCGCTTCGCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGT  
GGACGCTGGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTC  
AGTGGCATCCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGAC  
CATCCCCGCCAGCATTGCCAGCTCAGGGCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCAAGATTGAAG  
CGCTGCGCTGGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCCG  
CTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTA  
CATCGTCATCGACGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGC  
CACAGGTGGTCACAGATGTGGGCGTGACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTC  
CTCAACAGCCTCAAGAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCA  
CTCCATCTTCAGCCTCCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCA  
TCAGCTTCCAGCACCTGCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAG  
ATCGGCAACCTCACCAACCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTT  
CTACTGCCGCAAGCTGCGCTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCCTGCCGACATCGGCCTCC  
TGCAGAACCTCCAGAACCTAGCCATCAGGCGCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGG  
AAGCTGCGGGCCCTGCACCTGGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGTGGGCGAGCTGACCAACCT  
GACGCAGATCGAGCTGCGGGGCAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGC  
GCAGCGCTTGGTGGTGGAGGAGCCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCT  
GACAAGGAGCAGGCCCTGAGCGAGGCCGCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGG  
AGGGGCGAGGCCCTAGCTTCTCCAGAACTCCCGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGAGCTGGGGCC  
GCTTGTGAGTCAGGCCAGAGCGAGAGGACAGTATCTGTGGGGCTGGCCCCCTTTTCTCCCTCTGAGACTCACGTC  
CCCCAGGGCAAGTGCTTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTG  
GAGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCTGGGACCCTCACTTTAGTTCTTGGTATTTAT  
TTTTCTCCATCTCCACCTCCTTCATCCAGATAACTTATACATTCCCAAGAAAGTTGAGCCAGATGGAAGGTG  
TTCAGGGAAGGTGGGCTGCCTTTTCCCCTTGTCTTATTTAGCGATGCCGCGGGCATTTAACACCCACCTGG  
ACTTCAGCAGAGTGGTCCGGGGCGAACCAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTG  
CGGTCCACGGGAGAGCAGGCCTCCAGCTGGAAAGGCCAGGCCTGGAGCTTGCCTCTTCAGTTTTTGTGGCAGTT  
TTAGTTTTTTGTTTTTTTTTTTTTTTAAATCAAAAAACAATTTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTT  
GGGTATTAAGAAAGAAAAAAACTTAAAAAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGG  
GTGGCAGTTTCCCTTGAGCAAGCAGCCAGACGTTGAAGTGTGTTTCCCTTCCCTGGGCGCAGGGTGCAGGGTG  
TCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTTCTATTTGTTTCCCTGGGAGGGAGGTTTTTTTGTGTTTTT  
TTGGGTTTTTTTGGTGTCTTGTCTTCTCCTCCATGTGTCTTGGCAGGCACTATTTCTGTGGCTGTGCGG  
CAGAGGGAATGTTCTGGAGCTGCCAAGGAGGAGGAGACTCGGGTTGGCTAATCCCCGGATGAACGGTGCTCCA  
TTCGCACCTCCCCCTCCTCGTGCCTGCCCTGCCTCTCCACGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGC  
CCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGTCCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAG  
CCCTGTGCGCACCTGGTCCCTCATGAAGAGCAGACACTTAGAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGG  
AGGGCAGGCGTTGGTTCCAAGCGGTTCCCGTCCCTGGCGCTGGAGTGCACACAGCCAGTCGGCACCTGGTG  
GCTGGAAGCCAACCTGCTTAGATCACTCGGGTCCCCACCTTAGAAGGGTCCCCGCTTAGATCAATCACGTGG  
ACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGTCCATCCGTCTGCTCCGCTCATTGTGTTTTCT  
GCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAGCCTCTGACAACCATGAAGCAAAAATCCGTT  
ACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAAATCTATAACAGAAAAA

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**FIGURE 124**

MRQTIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
REAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEI DLKDNNLKTIEEIIISFQ  
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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**FIGURE 125**

GTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCAGAACCTGACAAAAAAGAAGAAAAAGAAGA  
AAAAAATC**ATG**AAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACCTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTT**TGAT**GTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

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**FIGURE 126**

MKTIQPKMHNSISWAI FTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTLCQCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHNTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

**Important features:****Signal peptide:**

amino acids 1-28

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**FIGURE 127**

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGCCGCGCCAC  
GCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCCGGGCCCGCGCCCCGCGCCCCGCGCCAGGTGAGCGCTCCG  
CCCCCGCGGAGGCCCGCCCCGGCCCCCGCCCCCGCCCCGGGCCGGGGGAACCGGGCGGATTCTCGCG  
CGTCAAACCACCTGATCCCATAAAACATTATCCTCCCGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGC  
CGCCGCGCCCTCGCCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGA  
GCGGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCCGGGCGTAGCGGCGCGCCTGGATGCGGACCCG  
GCCGCGGGGAGACGGGCGCCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCAACCCCTACGATGAA  
GAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCAT  
GCCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTG  
CCCGTGGGCATCCCTGCTGCCAGCCAGCGCATCTTCTGACGGCAACCGCATCTCGCATGTGCCAGCTGCCAG  
CTTCCGTGCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGCGGCTGCCT  
TCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCTGCCACA  
TTCCACGGCCTGGGCCGCTACACACGCTGCACCTGGACCCTGCGGCCTGCAGGAGCTGGGCCCCGGGGCTGTT  
CCGCGGCCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTCC  
GCGACCTGGGCAACCTCACACACCTCTTCTGACGGCAACCGCATCTCCAGCGTGCCCCGAGCGCGCCTTCCGT  
GGGCTGCACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCCTTCCGTGA  
CCTTGGCCGCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCACTGAGGCCCTGGCCCCC  
TGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCCACTCTGGGCC  
TGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCT  
CAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCA  
GGGCCACCGATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTG  
GAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTGACAGCCCCGCCGGGCAA  
CGGCTCTGGCCCACGGCACATCAATGACTCACCCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCCGCTCACTG  
CAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTCACGC  
AAGAACCGCACCCGCAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGG  
CTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTG  
GGCCTGCTGACACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCA  
CGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCTCCCTGATGGACGCCTGCCGCC  
CGCCACCCCCATCTCCACCCCATCATGTTTACAGGGTTTCGGCGGCAGCGTTTGTTCAGAACGCCGCCTCCAC  
CCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGC  
TCTTTTCTTAAAAAA

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**FIGURE 128**

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHG NRISHVPA  
ASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPATFHGLGRLHTLHLDR CGLQELGPG  
LFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHG NRISVPERAFRGLHSLDRLLHQN RVAVHVP HAF  
RDLGRLMTLYLFANNLSALPTEALAPLRALQYLR LNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGR  
DLKRLAANDLQGC AVATGPYHPIWTGRATDEEPLGLPKCCQPDAADKASVLEPGRPASAGNALKGRVPPGDSPP  
GNGSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGTGDS  
EGSGALPSLTCSLTPLGLALVLWTVLGPC

**Important features:****Signal peptide:**

amino acids 1-26

**Leucine zipper pattern:**

amino acids 135-156

**Glycosaminoglycan attachment site:**

amino acids 436-439

**N-glycosylation site:**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425



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**FIGURE 129**

GC GCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACATGGCTGCAGCCAC  
CTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTGCGAGGCGCCCGGCCCGCCCGGAGCCAA  
GCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCC  
TACTATGTTGGAACCTTGGGGACTCACACTGAGATCAAGAGAGTGGCAGAGGAAAAGTCACTTTGCCCTGCCA  
CCATCAACTGGGGCTTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAA  
AAGTGGTGATCACTTACTCCAGTCGTCTGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCCTTT  
GCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGCCAGTGATGAGGGCCGGTACAC  
CTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCATGTCATCTTAAAGTCTTAGTGAGACCATCCAAGC  
CCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACA  
GAGCCCATTTGTATTACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAG  
GATTGACTACAACCCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTACCAGTGCA  
CAGCAGGCAACGAAGCTGGGAAGGAAGCTGTGTGGTGCGAGTAAGTGTACAGTATGTACAAAGCATCGGCATG  
GTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTTGGTGTGGCTGCTAATCCGAAG  
GAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCC  
GTCTTGTGAAACCCAGCTCCTCTTCTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCACTCGCTCCACA  
GCAAATAGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGC  
ATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAG  
AAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCTGAATTACAATGGACTTGACTCCC  
ACGCTTTCCTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACAGAT  
GAGAGGTCATCTAAGTAGCAGTGAGCATTGCACGGAACAGATTGAGATGAGCATTTCCTTATACAATACCAA  
CAAGCAAAAGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAG  
CAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAA  
AACTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAATTTTCAAGAGGAAATGGGATGCTGTTTGTA  
AATTTTCTATGCATTTCTGCAAACTTATTGGATTATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTAT  
TACACCTGTCTACACCATGTACTGAGCTAACCACCTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATT  
CTGACTTAACTTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAG  
AGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAACTATGAAAGGAGACA  
AAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAA  
ATATATAATGGAGCAATTGTGGATTTCCCTCAAATCAGATGCCCTCTAAGGACTTTCCTGCTAGATATTTCTGG  
AAGGAGAAAATACAACATGTCATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAGGGATCTAGGAAT  
GCTGAAAGATTACCCAACATACCATTATAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCA  
CCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAG  
AGCGGGACTCCGTCTC

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**FIGURE 130**

MSLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVITYSSRHVYNN  
LTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVILKVLVRPSKPKCELEGELTEGSD  
LTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVR  
VTVQYVQSIGMVAGAVTGIVAGALLIFLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRS  
SRSGSSSTRSTANSASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

**Important freatures:****Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

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**FIGURE 131**

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC  
AGTCCACAGAACCGTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA  
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTCTTTTGGGCTTATCTCTGGCG  
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC  
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTAGGGTTG  
TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG  
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGACAGATCTCTG  
AGGACAGTCCGGTAGGCTTCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC  
AACGGAGAGATTTCTTATTTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
CAATCCCTTGACAGGAGAAATTGAACATAAAAAACAACCTCGATTTGAAAAACTTCAGTCCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
ACCTGAGAACGCGCCTGAACTGTGGTTGCACTTTTTCAGTGTTTCAGATCTTGATTACAGGAG  
AAAATGGGAAAATTAGTTGCTCCATTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA  
AACTTTTACACCCTACTAACGGAGAGACCCTAGACAGAGAAAGCAGAGCGGAATACAACAT  
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTCTGTC  
CGCGAGAACAACAGCCCCCGCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCCCAGGTCACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCCCTACAT  
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG  
CGAGGCGCTGGTGCGCGTGGTGGTGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGGCGGAGCCGGGCTAC  
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTGGTCAAGGAC  
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
CCAGCCCTACCTGCCTCTCCCGAGGCGGCCCGACCCAGGCCAGGCCGACTTGCTCACCG  
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTC  
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTTGGTGCCCGA  
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCTATCCCAGAGCTACC  
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCTGAAGCCGATT  
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA  
TAACTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT  
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTTCTT

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**FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314  
<subunit 1 of 1, 798 aa, 1 stop  
<MW: 87552, pI: 4.84, NX(S/T): 5  
MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLNEKLDREDLCGHTEPCVLRVFQVLLESFFEFFQAELOV  
IDINDHSPVFLDKQMLVKVSESSPPGTTTFPLKNAEDLDVGQNNIENYIIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVDVTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAEVMTSAFTSPIPENAPETVVALEFSVS  
DLDSGENGKISCSIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ  
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT  
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

**Important features:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

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## FIGURE 133

[illegible]

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**FIGURE 134**

MT PQSLLQTTLFLLSLLFLVQGAHGRGHREDFR FCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRD FLLSDKASSLLCFQH  
QEESLAQG PPLLATSVTSWWSPQNISLPSAASFTFSFHSP PHTAAHNASVDMCELKRD LQLL  
SQFLKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTK VANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVV SALACLVTIAAYLCSRVP LPC  
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPI ILAVHRTPEGVIY  
PSMCWIRDSLVS YITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVL TLLGLSLVLG  
LPWALIFFSFASGTFQLVVL YLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSN SDSARLP  
ISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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**FIGURE 135**

GCCTAGCCAGGCCAAGAATGCAATTGCCCGGTGGTGGGAGCTGGGAGACCCCTGTGCTTGGACGGGACAGGGTCGG  
GGGACACGCAGGATGAGCCCCGCGACCACTGGCACATTCTTGCTGACAGTGTACAGTATTTTCTCCAAGGTACA  
CTCCGATCGGAATGTATACCCATCAGCAGGTGTCTCTTTGTTTCATGTTTTGGAAAGAGAATATTTAAGGGGG  
AATTTCCACCTTACCCAAAACCTGGCGAGATTAGTAATGATCCCATAAACATTTAATACAAATTTAATGGGTTAC  
CCAGACCGACCTGGATGGCTTCGATATATCCAAAGGACACCATATAGTGATGGAGTCCTATATGGGTCCCCAAC  
AGCTGAAAATGTGGGGAAGCCAACAATCATTGAGATAACTGCCTACAACAGGCGCACCTTTGAGACTGCAAGGC  
ATAATTTGATAATTAATATAATGTCTGCAGAAGACTTCCCGTTGCCATATCAAGCAGAATTCTTCATTAAGAAT  
ATGAATGTAGAAGAAATGTTGGCCAGTGAGGTTCTTGGAGACTTTCTTGGCGCAGTGAAAAATGTGTGGCAGCC  
AGAGCGCCTGAACGCCATAAACATCACATCGGCCCTAGACAGGGGTGGCAGGGTGCCACTTCCCATTAATGACC  
TGAAGGAGGGCGTTTATGTCATGGTTGGTGCAGATGTCCCGTTTTCTTCTTGTGTTTACGAGAAGTTGAAAATCCA  
CAGAATCAATTGAGATGTAGTCAAGAAATGGAGCCTGTAATAACATGTGATAAAAAATTTGTAATCAATTTTA  
CATTGACTGGTGCAAAATTTTATTGGTTGATAAAACAAAGCAAGTGTCCACCTATCAGGAAGTGATTTCGTGGAG  
AGGGGATTTTACCTGATGGTGGAGAATACAAACCCCTTCTGATTCTTTGAAAAGCAGAGACTATTACACGGAT  
TTCCTAATTACACTGGCTGTGCCCTCGGCAGTGGCACTGGTCTTTTTCTAATACTTGCTTATATCATGTGCTG  
CCGACGGGAAGGCGTGGAAAAGAGAAACATGCAAACACCAGACATCCAAGTGGTCCATCACAGTGCTATTGAGA  
AATCTACCAAGGAGCTTCGAGACATGTCCAAGAATAGAGAGATAGCATGGCCCTGTCAACGCTTCCTGTGTTT  
CACCTGTGACTGGGGAAATCATACCTCCTTTACACACAGACAACATGATAGCACAAACATGCCATTGATGCA  
AACGCAGCAGAACTTGCCACATCAGACTCAGATTCCCCAACAGCAGACTACAGGTAAATGGTATCCCTGAAGAA  
AGAAAACTGACTGAAGCAATGAATTTATAATCAGACAATATAGCAGTTACATCACATTTCTTTCTCTTCCAAT  
AATGCATGAGCTTTTCTGGCATATGTTATGCATGTTGGCAGTATTAAGTGTATACCAAATAATACAACATACT  
TTCATTTTACTAATGTATTTTTTTGTAATTAAGCATTTTTTGACAATTTGTAAACATTGATGACTTTATATTT  
GTTACAATAAAAGTTGATCTTTAAATAAATATTATTAATGAAGCCTAAAAA

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**FIGURE 136**

MQLPRWWELGDPCAWTGQGRGTRRMSPATTGTFLLTVYSIFSKVHSDRNVYPSAGVLFVHVLEREYFKGEFPPY  
PKPGEISNDPITFNTNLMGYPDRPGWLRYSIQRTPYSDGVLYGSPTAENVGKPTIIETAYNRRTFETARHNLII  
NIMSAEDFPLPYQAEFFIKNMNVEEMLASEVLGDFLGAVKNVWQPERLNAINITSALDRGGRVPLPINDLKEGV  
YVMVGADVFPSSCLREVENPQNQLRCSQEMEPVITCDKKFRTQFYIDWCKISLVDKTKQVSTYQEVIRGEGILP  
DGGEYKPPSDSLKSRDYYTDFLITLAVPSAVALVFLILAYIMCCRREGVEKRNMQTPDIQLVHHSIAIQKSTKE  
LRDMSKNREIAWPLSTLPVFHPVTGEIIPPLHTDNYDSTNMPLMQTQONLPHQTQIPQQQTGKWYP

**signal sequence:**

Amino acids 1-46

**transmembrane domain:**

Amino acids 319-338

**N-glycosylation site:**

Amino acids 200-204

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 23-27

**Tyrosine kinase phosphorylation site:**

Amino acids 43-52

**N-myristoylation sites:**

Amino acids 17-23;112-118;116-122;

185-191



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**FIGURE 137**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT  
GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG  
GAGTGTGTGGAACAGGACCCGGGACAGAGGAACC**ATGG**CTCCGCAGAACCTGAGCACCTTTT  
GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG  
GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAGGCTTATAGGAACTAGCCCTGCA  
GCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG  
CTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA  
GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT  
TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA  
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAAGTGCAATTGTCGGCAAGAGAT  
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT  
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT  
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TG**AGAGTG  
AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
TTGTGTGTGTTTTTGTGTTTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA  
TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC  
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGT  
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
GTTGTTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG  
TTATTTTTTA

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**FIGURE 138**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQAEKFDLGAAY  
EVLSDSEKRKQYDTYGEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEVTLEEVYAG  
NFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVVCDECPNVKLVNEERTLEVEIEPGVVDGMEY  
PFIGEGERPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPG  
AKLWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLOQY

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

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**FIGURE 139**

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGCGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCTGTCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 140**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405  
<subunit 1 of 1, 125 aa, 1 stop  
<MW: 13115, pI: 5.90, NX(S/T): 1  
MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

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**FIGURE 141**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
CGCCTCTCCGCACG**ATG**TTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC  
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGGCCCTCCCCGTGCCTGCCCCCAGAG  
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACCCTGGCAGTGCTGGT  
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA  
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGGCGGC  
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGGAGCTGGGCTCCAGCTTTTCC  
GCCCCCTCGGAATCACAACTGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGG  
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC  
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
AGCT**AG**AGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCCTGTCCG  
GGACCCCCCTGCCTTCTGCTCACCCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG  
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCTACTCTGACCTCCTTCACGTGCCC  
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
><subunit 1 of 1, 327 aa, 1 stop  
><MW: 37406, pI: 9.30, NX(S/T): 1  
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSSLGFFSLLWLQLSCSGDVARAVR  
GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI  
TTGYKTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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**FIGURE 143**

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAGTTGCCTCATCGCAGGCAGATGTTGGGG  
CTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAA  
AAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACC  
ATAACTTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATTTCAGGAATTGTAGGGCCTCAACCTATA  
GACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATC  
TGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAATGTGATTTTCT  
ACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAACTTTTGGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCAT  
GAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATG  
ATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTT  
TCAGAAGATTGTGATTTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTA  
TCTTGACTATAAAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTT  
TTGTTGCAAACCTGACGGAATGGAAACGACAGAATATAACTAACCACTGGAAAAATGGATGAACTCAATGTA  
GAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACACCTCCTCTGCTTATCGTATTTTATCAACA  
GCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTACCTCAGT  
TTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGAT  
GTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAA  
CATAAAGTGAACAGAAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCATGGGAAG  
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACA  
AACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGT  
GTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGATAAT  
TCAAACTGCTGTTGGTTTTAATTTTGTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTC

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**FIGURE 144**

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR  
QEEIPVVIAASEDRLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK  
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT  
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA  
NLTEWKRONITNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRHLGS  
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK



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**FIGURE 145**

AAACTTGACGCCATGAAAGATCCCGGTCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT  
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACCTCCAATAAAACATTTTCCATCCAAA

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**FIGURE 146**

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE  
FLNWHALFESIKRKLPFLNWDAPFKLKGLRSATPDAQ

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**FIGURE 147**

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT  
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAA

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**FIGURE 148**

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS  
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN  
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

**Signal Peptide:**

amino acids 1-20

**N-myristoylation Sites:**

amino acids 67-72, 118-123, 163-168

**Flavodoxin protein homology:**

amino acids 156-174

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**FIGURE 149**

GGCACGAGCCAGGAAGCTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC  
**ATG**GGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG  
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTTCCCCAAAG  
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC  
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT  
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT  
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA  
GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG  
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG  
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC  
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA  
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG  
GGGTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC  
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGTTTGGG  
GTTTCATGCAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 150**

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELNANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

**Signal Peptide:**

amino acids 1-18

**N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

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**FIGURE 151**

GCGTGGGG**ATG**CTAGGAGCTCGAAGGTGGTGGTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA  
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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**FIGURE 152**

MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS



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**FIGURE 153**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACCTCCCTATGGAAGTAGACATATTCGCCCTTGCTTTAAAGGTCTGATCACTT  
ATATCTGGAACCAAAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTTGGACAATTCAGTGTGGACTTCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTTCAGTGGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTGTCAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTCTGA  
ACTAAGTGAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAA

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**FIGURE 154**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCSLKCQ
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPFS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKL PVEAKLPWFKQAQEEGA AVSEEPS
```

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

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**FIGURE 155**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGGAGGACAGGG  
AGTCGGAAGGAGGAGGACAGAGGAGGGGCACAGAGACGCAGAGCAAGGGCGGCAAGGAGGAGACCTGGTGGGAG  
GAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAGGGGCCCTGGCCTGCCTCCTGCTGGCC  
CTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGC  
CCTTGGACATGGCCTGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAG  
CTGGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCA  
GGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGA  
GATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTG  
GCCACAGTGGTGCTTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGC  
CAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAACTCAGCAGGCAGCTTTGGAAT  
GAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAATTTGGGACCAACACTCAGGGAG  
CTGTGGCCCAGCCTGGCTATGGTTTCACTGAGAGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCCACCCTCT  
GGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAA  
TGGTGACAACAACAATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCA  
GCAGTGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCC  
TGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACCCGGGTG  
TGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTGAGGGCTTCAGAGGACAGGGAGTTTCCA  
GCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTGGAGGCTCTGGAGACAATTATCGGGGGCAAGGG  
TCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTTGGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGAT  
GTTTAACTTTGACACTTTCTGGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGG  
ACCAGAGAAGCTCTCGCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACTCCCT  
CCTTAAACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAAAAA  
AA  
AA

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**FIGURE 156**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212  
><subunit 1 of 1, 440 aa, 1 stop  
><MW: 42208, pI: 6.36, NX(S/T): 1  
MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA  
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG  
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM  
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS  
GSQSGSSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSSGSSSSGSSSGSGSGSGSGSGSGSSG  
GSSTGSSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRRQGVSSNMREISKEGNRLL  
GGSGDNYRGQGSWSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ  
RSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
383-389, 387-393, 389-395, 395-401**Cell attachment sequence.**

amino acids 301-304

FIGURE 157

[illegible]

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**FIGURE 158**

MDFLLLGLCLYWLLRRPSGVVLCILGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHNLSGLLGLSLRY  
NSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQITQLPNTTFRMPNLRSDLSYNK  
LQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSKFLDIGYNQLKSLARNSFAGLFKLTLEHNDLV  
KVNFAHFPRLISLHSLCLRRNKVAIVVSSLDWVWNLEKMDLSGNEIYMEPHVFETVPHLQSLQLDSNRITYIE  
PRILNSWKSLSITLAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAAPT  
SGHLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLIVVL  
VLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVIINEYGSCTCHQPAR  
ECEV

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**FIGURE 159**

CAGAGAGGAGGCTTTGGGAATTGTCCAGCAGAAACAGAGAAGTCTGAGGTGGTGTCAAGACA  
AAAG**ATG**CTTCAGCTTTGGAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCT  
CTTCTTGACAATCTTGGAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCA  
CGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAACTGAAGGTGACCC  
TAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCAGGAAGCTGAG  
AAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAATAACACGGACATTTTTGGGTTGAA  
AATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTA  
ACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATC  
AACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAACTGATCCCCAGACACA  
CCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGC  
TGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGC  
ACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCT  
GGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCC  
TCATCT**TGA**AGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCT  
TGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAA  
AGCCTGAGTCCCACCAGAAGGACCTTCCAGATACCCCCTTCTCCTCACAGTCAGAACAGCAG  
CCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCACCCTTAA

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## FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59622
><subunit 1 of 1, 249 aa, 1 stop
><MW: 27011, pI: 5.48, NX(S/T): 2
MLQLWKLVL LCGVLTGTSESLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV
DLGVLQKSSAWQLAKQKAQEA EKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDG
KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECA SDPTS
ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV DNPQ
HKTQLQTLI
```

**Important features:**

**Signal peptide:**

Amino acids 1-15

**N-glycosylation sites:**

Amino acids 124-128;132-136

**N-myristoylation sites:**

Amino acids 12-18;16-22;26-32;101-107;122-128;141-147

**Leucine zipper pattern:**

Amino acids 44-66



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**FIGURE 161**

CAGCCACAGACGGGGT**CATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTTCTGACCTGTCAATCGGGGGACCACCATTATGACACACGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC  
CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT  
GAGCATTCAGGGCTGCGTGAGGCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGGTTTGCCCTTCCTGCT**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA  
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

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**FIGURE 162**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847
><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLM
LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW
APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCM
PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEV
GQVCQETLLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLN
SASSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG
GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGV
GLALAPALWWGVVCPSC
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-15

**Transmembrane domain:**

Amino acids 243-260

**N-glycosylation sites:**

Amino acids 46-50;189-193;382-386

**Glycosaminoglycan attachment sites:**

Amino acids 51-55;359-363

**N-myristoylation sites:**

Amino acids 54-60;75-81;141-147;154-160;168-174;169-175;  
198-204;254-260;261-267;269-275;284-290;333-339  
347-353;360-366;361-367;388-394;408-414;419-425

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**FIGURE 163**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTGAGAAGAGCCAC  
AGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGGCCCTTCGAGGAGCTTCTGCATTGCTGGTT  
CTGTTTCCTTGAGCTTTTCTGCCCCCGCCGAGTGTACCCAGGAGCCAGCCATGGTGCAATTACATCTACCAGCG  
CTTTTCGAGTCTTGGAGCAAGGGCTGGAAAAATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCGAAGAGT  
TCTCAAAAAATATATCTGTCTGCTGCTGGGAAGATGTGAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAAAC  
TTGGCACTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTGACGAGTGCAT  
CGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAAGATCCGGACTCTGC  
TGAATGCAAGCTGTGACAAACATGCTGATGGGCATAAAGTCTTTGAAAATAGTGAAGAAGATGATGGACACACAT  
GGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGT  
TTGGGAATTTGCAAACATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACAC  
TTTCCTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTCTATTTTTTATAACCAAGCAACTTCTAATGAG  
ATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCAGGAGGGGTAGGCCGAGCATT  
GGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCTCTGGGCCATCCACTCTG  
GGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTTCATGGGAT  
ACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATTCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGG  
GGGCCAGGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACT  
TGTTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGATAAGCAGCTCTATGCCTGG  
AATGAAGGAAACCAGATCATTACAAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAATGCATTACAGCTGT  
GAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGCCCTTCACAATATAGTATCC  
CTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATACGTATGCCTCCTTTCCCAATGTCACTGCCTTAG  
GTATCTTCCAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAACCTC  
CTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTGTTTACTGCTCCCCAGCATTAC  
TGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCTAATATTACCACTGGCTTTTCTCT  
CCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTCAAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACT  
AAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTGTGAGACAAGGTCTCACTATGTTGCCAGGCTGGT  
CTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCACCA  
CACCTGGCTTAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCTTAGCCCTGTCTTCCACTAAGCTT  
GGTAGATGTAATAATAAAGTGAAAAATATTAAACATTTGAATATCGCTTTCAGGTGTGGAGTGTGTCACATCAT  
TGAATTCCTCGTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGTAACA  
CAATTACAAAGTGAAAGATACAGCTAGAAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCA  
AATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC  
TTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCCTCCAGAAAACAGTC  
TAAGGGTGAGGACCCCAACTCTAGCCTCCTCTTGTCTTGCTGTCTCTGTTTCTCTTTCTGCTTTAAATTCA  
ATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

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**FIGURE 164**

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVRVLEQGLEKCTQATRAYIQEFQEFKSNISVMLGRC  
QTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQEAEKKIRTLNASCNDMLMGI  
KSLKIVKKMMDTHGSWMKDAVYNPKVYLLIGSRNNTVWEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYK  
GFLFFHNQATSNEIIKYNLQKRTVEDRMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLT  
IEPGTLGVEHSWDTPCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSM  
IHYNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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**FIGURE 165**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGCAGTGTGTTTGCC  
TTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTCCTAGTAACTGTGTCTGACTGTG  
CTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTT  
CGAGGGCTGCGGATGTGCACCCCGCTGGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTT  
CTTCAGGAAACGCAAGCACCACACCTGTCTTGTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGT  
ACCGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCTGGTCTCAGGATACCCACCATCCTTTT  
CCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGACTCTCCCAGTCCCTACACTGACT  
ACCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATACTCCCATCATGACATGGTCCCCAG  
GCTGGCCTGAGGATGTACAGCTTGAGGCTGTGGTGTGAAAGGTGGCCAGCCTGGTTCCTTCCCTGCTCAGGC  
TGCCAGAGAGGTGGTAAATGGCAGAAAGGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTTTCCCTGGGC  
CCTGCCCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCCTGGGCACAGGCTCTTGGGTGCATTGCT  
CAGAGTCCCAGGTCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGTAGTTCA  
TCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTTCCCAGAGGGCAGCAGAC  
AGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCT  
GTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCAGAATTGTATGCCTCTGAGGCCCCCTCTTACCACACTTT  
ACCAGTTAACCCTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAATCTAAT  
CTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCAAGGATCAGCCCTGAGAGC  
AGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGCAGGGCAGGG  
GCTGAAAGGGGCACTGATTGAGACCAGGGAGGCCAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAA  
CTGAAAAAA

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## **FIGURE 166**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEETCHPGSHKVPFFFRKRK  
HHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Important features:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

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**FIGURE 167**

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGGTGTGGAGCCC  
TCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTCCCTCATGTATGGCAAGAGCTCTACTCGTGCGG  
TGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTG  
CTGGAGGCTGTTAATGGGACAGATGCTCGGTTAAAATGCACTTTCTCCAGCTTTGCCCCTGTGGGTGATGCTCT  
AACAGTGACCTGGAATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCT  
TCCAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCCATC  
CTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCACCTGATGTTGATGG  
GGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCA  
TTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATTGTAGTGGTCCCTCTCCAGCATTACCGGAAAAAGCGA  
TGGGCCGAAAGAGCTCATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGT  
CTCTGTTTATTTAGAAGACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTA  
GTATTTCTTGAAGTTAATGGAACTTTTCTTTGGGCTTTTCCAGTTGTGACCCGTTTTTCCAACCAAGTTCTGCAGC  
ATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATATCACCAGTCATACACAGC  
CTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAG  
CTACATTTTTGCCCTTAAGACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATA  
AAAGCCAATTTGTCTGTTACATTTCTTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGT  
TTACTCTCTTTCTTCCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAACAGTAAA  
TCCTAAATTCAAACGTGTTAAATGACATTTTATTTTATGTCTCTCCTTAACTATGAGACACATCTTGTTTTAC  
TGAATTTCTTTCAATATTCCAGGTGATAGATTTTTTGTCG

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**FIGURE 168**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTWNFRPLDGGPEQ  
FVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVKNPPDVG VIGEIRLSVVHTVRF  
SEIHFLALAIGSACALMIIIVIVVVLFOHYRKKRWAERAHKVVEIKSKEERLNQEKKVSYLEDTD



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**FIGURE 169**

GAGCGAAC**AT**GGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCCAAGAAAGAAGGAGATGGTGTTATCTGA  
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
CTCCAACCTGCATAGACAGTGTGTGCTTTGCAAGCAAGCTGATGAAGAATTCAGATCCTGGC  
AAACTCCTGGCGATACTCCAGTGCATTCACCAACAGGATATTTTTTGGCATGGTGGATTTTG  
ATGAAGGCTCTGATGTATTTTCAAGATGCTAAACATGAATTCAGCTCCAACTTTCATCAACTTT  
CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
TGAGCAGATTGCCCCGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
CAAATTATGCTGGTCCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG  
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC  
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGT  
GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCTTTTATG  
TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
CCATACAGCTTTCTGATGAGT**TAAAA**AGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC  
CTCTTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAAGAAGATGTGTAGTGCCTTA  
ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
CCCAGTGAACTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA  
CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT  
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC  
TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATATGTGTGTCATGTGGTCTTCTGAAAATG  
GAACACCATTTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA  
GATTTTCAAGATTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAA  
TAGCTTAGTGCTAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
CCAGGCGCAGTGAATACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
GAGGTGAGGAGTTCGAGACCATCCTGGCCAAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC  
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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**FIGURE 170**

MAARWRFWCVSVTMVVALLVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPFVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFINFPKKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLA VIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSI FRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

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**FIGURE 171**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTTTCTGCATCTCC  
AGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGATGCTGTGCCAGCCACACAAGAG  
ATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTTGCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCC  
AGACGTGTGGAAACTGCACCTTCAGAGTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATA  
AACCAGAACTGCGACTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGCAGTGTCAGCTTAATGGAACATCAGGGG  
AACGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAAGAGGCTGGTGTACCTGAGATCTGGGATGC  
TGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATTCTGTGACCTGTCTGAGGCCAC  
CCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAGAATTCTGGACAGCATGAGATGCGTGTGCTGATGG  
GGGCCAGGGACTCTGAACCCTCCTGATGACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTG  
GGGAACCCTTCACCCTTCTGTGAGATTTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATC  
ATAATAAATTTATGTACTTTATAAATGAAAA

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**FIGURE 172**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPLARTQTCGNCTF  
RVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Important features:**

**Signal peptide:**

amino acids 1-24

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**FIGURE 173**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGCGAGCGCTCACTCGCTCGCACTCAG  
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAGTTCCTCT  
GCGCGTCCGACGGCGAC**ATG**GGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG  
CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGGCAGAACGTCAACCTCACCTGCAGGCTCT  
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG  
GATAGCGGCCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGGT  
CCATGGTGGCATGGAGCTGCAGGTGCAGACAGGCCAAAGATGCACCATCCAACCTGTGTGGTGT  
ACCCATCCTCCTCCCAGGATAGTGAACACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
CTCCAACCGCCGTGCCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAACC  
CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG  
TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC  
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCTGTCCCTGACT  
CTCCAAACTTTGAGGTCATCT**TAG**CCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCCAGCCCCCTCAACCCCTC  
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCGTGTTCCAAGGATTTTGGGGTGCTGAG  
ATTCTCCCTTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGGCACGGTG  
GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTGGCCGAGGCTGCTCTTCTGTC  
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
ATGTTGCCCCACCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCTACTCCCACTGCTCAGCGCGGGCC  
ATTGCAAGGGTGCCACACAATGTCTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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**FIGURE 174**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFQVATPYSLYVCPEGQNVTLTCRLLGPVVK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLTLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQQRQAASNRRQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPFPGPDVFFPSLDPVPDSPNFEVI
```

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

FIGURE 175

[illegible]

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**FIGURE 176**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLATLQEAATTQENV  
AWRKNWMVGGEGGASGRSP

**Important features:**

**Signal peptide:**

amino acids 1-18



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**FIGURE 177**

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGGCCGGGGAGGGGAACTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCC**ATG**AGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTG  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCCTTCCTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGA  
CTCG**TGA**CTGCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCCTCCTCCTCCTCCTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACAAATAAAAATGAAACGTG

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**FIGURE 178**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLASADGTLCPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

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**FIGURE 179**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT  
CCGTACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC  
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTCTTCAGGGGCCAGTTCTCTAGCGTG  
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
ACAAACTGGTGAAGGATTCTATTGCGGAGGGGGCGCATCTCTCTGAGGCTGAAAACATTAC  
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA  
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTT  
GATAGAGACATCCAGCTACTCTGTCACTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG  
GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA  
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACTGGAC  
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC  
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATGTAACCCATA  
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG  
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGACTATGAGTG  
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT  
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAATCCC  
ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
TCAGGAATTTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTTCATTATATTACACTTTCAGTA  
AAAAAA

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**FIGURE 180**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRIS SQSYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFP RP TAKWKGPQGQDLSTD SRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAE LDWRRKHGQAE LR D ARKHAVEVTLD PET AHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRTRKSVVASQS FQAGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLS  
PDHGYWVLRLNGEHL YFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATT PFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

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**FIGURE 181**

CGCATGGTGCGCCCGGTGGCGGTGGCGGGCGGCGTTGCGGAGGCTTCCTTGGTGGATTGCAACGAGGAGAAGA  
TGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGG  
CGGCCTCGCCCTGTTGTGCTGCGCCGCGCCGCGCCGCGCCGCTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCG  
GTGGCGGCGGGGCGCGGGGACAGGTGGACGCGTCGCCGGGCCCCGGGTGCGGGGCGAGCCACGCCACCCCTTC  
CCTAGGGCGACGGCTCCACGGCCCCAGGCCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGC  
TGCGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTCCACCACCTTTT  
AGGCGCGGCTCGGCCCCCTCGCCGACCACCCCTCCGGCGGGGAAACGCACTTCGACCACCTCTCAGGCGCCGACC  
AGACCCGCGCCGACCACCCCTTCGACGACCACTGGCCCCGCGCCGACCACCCCTGTAGCGACCACCGTACCGGC  
GCCACGACTCCCCGACCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTG  
CCACCGAGGCCCCCTCTTCGCCTCCTCCAGAGTATGTATGTAAGTCTGTGGTGGAGCCTGAATGTGAAT  
CGCTGCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAAGA  
GGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCATGTGACTGTAGTCCACATGGAGCTCTCAGCATAC  
CGTGCAACAGGTAAAGCAACAGAGGGTGGAACTGAAGTTTATTTTATTTTAGCAAGGGAAGGCTGCTA  
CTCTCAAGGACCATACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAATATTTTATATACTTTTA  
TTCTCTTACTTTATATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAG  
CACTAGAGTCGCCAATTTTCTCTGGGATAATTTCTGTAAATTTCTAGGGAAGGAAATATTTGAAGAATAAATCT  
GCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATACCA  
TTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTAATCAAAATCTACATTTGTTTCTTTGGACA  
TCTAAAGCTTAACCTGGGGGTACCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAG  
TACATTTTGTAGACCAAAAGTAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAAT  
CTAGTGAATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTTATCTTTGACCTTATG  
TGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAATAATGAAAAAATAATG  
ACAGGTTATACTCAGTGTAACTGGGTATAACCCAAGATCTGCTGCCACTTACGAGCTGTGTTCCCTTGGGCAAG  
TAATTTCTTTTCACTGAGCTTGTTTCTTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAATGC  
CTAGCACATGTCACTCAATAAATTTCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACA  
TGTTTTAAGAACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTATA  
AATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAGAGGCTGGGCGCGGT  
GGCTCAGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGATCACTTGAGGCCAGGAGTTCTAGATGA  
GCCTGGCCAGCACAGTGAAACCCGTCTCTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCT  
GTAGTCCCAGTACTCGGGAGGCTGAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGA  
GATCGGCCACTGCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952  
><subunit 1 of 1, 258 aa, 1 stop  
><MW: 25716, pI: 8.13, NX(S/T): 5  
MRSLSLGGGLALLCCAAAAA AVASAASAGNV TGGGGAAGQVDASPGPGLRGEP SHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSTTTGPAPTTVPATTVPAPTTPTPTDLPSSSNSSVLPTPPATEAPS  
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

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**FIGURE 183**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGTCTCGGTGCCCCA  
GGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCCCTGGTACGTGCTTGCGGTGGCC  
TCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGA  
AAACAACCTGCGGACGCTGTCCTCTCAGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGC  
GAAACTCCGGATGGGTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGA  
GACTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCTGAC  
GGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGCCTGGGCTTCCTGTACAGTAGC  
AGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGG  
CGCCACAGGGTCCTGTGACCTCGGCCAGTGTCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCT  
CAGAATAAAGCGATTCCACAGCA

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## **FIGURE 184**

MGGLLLAAFLALVSVPRQAVWLGRDLPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVTLTPENNLRTLSS  
QHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAII FTQLEFGDEPFNTVELYSLTETASQEAM  
GLFTKWSRSLGFLSQ

**Important features:**

**Signal peptide:**

amino acids 1-20



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**FIGURE 185**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACAGCAGCCAAGGA  
ACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATCCTGCTTGCTCTGGCAACAGGGC  
TTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAGTGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTG  
TTCGAGAAGACGCGGCTACTCTGTGGGGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCT  
CAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAG  
CCACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATGCTG  
GTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCACGCTGTGTCACTGC  
TGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCAGTTACGCCTGCCTCACACCTTGGCAT  
GCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTG  
TGTGCCAGCGTGCAGGAAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTC  
TCTTCAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCT  
GCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCATCACCC  
TCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAATAAGAAACCCTAAGCCAAGACCCTCTACGAACA  
TTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCT  
GGATTCAAATTCTGCCTTGAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCA  
GCCCCAAAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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## FIGURE 186

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQ  
HNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTITWAVRPLTLSSRCVTAGTSCSLISGWG  
STSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTMVCASVQEGGKDSCQGDGGPLVCNQLQGIISWGQD  
PCAITRKPVGVTYTKVCKYVDWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**  
amino acids 58-63

**N-glycosylation sites.**  
amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**  
amino acids 145-148

**Kringle domain proteins.**  
amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**  
amino acids 199-209, 47-63, 220-243

**Apple domain proteins**  
amino acids 222-249, 189-222

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**FIGURE 187**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG  
ACC**ATG**GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC  
CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACCTATGGTGGAAATTTCCCTTTATACC  
TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCA  
GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG  
GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG  
GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
CTTCCTCTTCCTTGAGGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
GAGAATCTCAAAGTCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT  
GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGGAAACCTCT  
ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
AATTCCTATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
CAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCGGCTCCCCCAATTCC  
CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA  
TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
GAAGTGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT  
TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA  
TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTGTTGCCATTGAGAGGGGAGACACA  
GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGAGAGTGTGGCGA  
AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
GTGATGCCACCCCCAAGTTGGACCAGGAGACTACGAGGCCAGTGTCCCCATCAGTGCCCC  
AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT  
CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC  
GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA  
TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG  
GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC  
CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTGCTGCAAC  
GTGGAGGGGAGTGCATGCGCAAGGTGGGCGCATGAAGGGCATGCCACGAAGCTGTGCGC  
AGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTACCC  
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG  
ACTGTCT**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT  
CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC  
TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTGGCCAATAATAAAGCCCCA  
GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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**FIGURE 188**

MVPAWLWLLCVSVPQALPKAQPAELSVFVPEVNYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH  
VYQQLSPEPEDGVEGRAFOVDPTSGSVTLGVLPPLRAGQNIILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADLEPAFRLMDFAIERGDTE  
GTFGLDWEFDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISTRFSLVNDSEGWLCIEKFSGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLRVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGTLLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 189**

[illegible]

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**FIGURE 190**

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRLTRIPSNLSSDT  
QVLLQLQSNNIAKTVDLQQLFNLTEDFSQNNFTNIKEVGLANLTQLTTLHLEENQITEMTDYCLQDLSNLQEL  
YINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDSTPNLEILMIGENPVIGILDMNFKPLANLRSLVL  
AGMYLTDPGNALVGLDSLESLSFYDNKLVKVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINN  
MGELVSVDRYALDNLPELTKLEATNNPKLSYIHRLAFRSVPALLESIMLNNNALNAIYQKTVESLPNLREISHS  
NPLRCD CVIHWINSNKTNIREFMEPLSMFCAMPPEYKGHQVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGTTVF  
LDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNVQGADTRVATIKVNG  
TLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPHITYTARVPVDVHEYNLTHLQPSTDY  
EVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETSTALAAVMGSMFAVISLASIAVYFAKRFKRKNYHHSK  
KYMQKTSSIPLNELYPPLINLWEGDSEKDKDGSADTKPTQVDTSRSYMW

**Important features:****Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 508-530

**N-glycosylation sites:**Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;  
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

**N-myristoylation sites:**

Amino acids 16-22;224-230;464-470;637-643;698-704

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**FIGURE 191**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGGAATCACGC  
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTTGTGAATAAACTTGATACACCA

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**FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675  
><subunit 1 of 1, 247 aa, 1 stop  
><MW: 25335, pI: 7.00, NX(S/T): 0  
MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVKGALDGINSGITHAG  
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGV NQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225



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**FIGURE 193**

GAAGTAGAGGTGTTGTGCTGAGCGGCGCTCGGCGAACTGTGTGGACCGTCTGCTGGGACTCC  
GGCCCTGCGTCCGCTCAGCCCCGTGGCCCCGCGCACCTACTGCC**ATG**GAGACGCGGCCTCGT  
CTCGGGGCCACCTGTTTGCTGGGCTTCAGTTTCCTGCTCCTCGTCATCTCTTCTGATGGACA  
TAATGGGCTTGGAAGGGTTTTGGAGATCATATTCATTGGAGGACACTGGAAGATGGGAAGA  
AAGAAGCAGCTGCCAGTGGACTGCCCCTGATGGTGATTATTCATAAATCCTGGTGTGGAGCT  
TGCAAAGCTCTAAAGCCCCAAATTTGCAGAATCTACGGAAATTTTCAGAACTCTCCCATAATTT  
TGTTATGGTAAATCTTGAGGATGAAGAGGAACCCAAAGATGAAGATTTTCAGCCCTGACGGGG  
GTTATATTCCACGAATCCTTTTTCTGGATCCCAGTGGCAAGGTGCATCCTGAAATCATCAAT  
GAGAATGGAAACCCAGCTACAAGTATTTTTATGTCAGTGCCGAGCAAGTTGTTTCAGGGGAT  
GAAGGAAGCTCAGGAAAGGCTGACGGGTGATGCCTTCAGAAAGAAACATCTTGAAGATGAAT  
TG**TAA**CATGAATGTGCCCCTTCTTTCATCAGAGTTAGTGTTCTGGAAGGAAAGCAGCAGGGA  
AGGGAATATTGAGGAATCATCTAGAACAATTAAGCCGACCAGGAAACCTCATTCCTACCTAC  
ACTGGAAGGAGCGCTCTCACTGTGGAAGAGTTCTGCTAACAGAAGCTGGTCTGCATGTTTGT  
GGATCCAGCGGAGAGTGGCAGACTTTCTTCTCCTTTTCCCTCTCACCTAAATGTCAACTTGT  
CATTGAATGTAAAGAATGAAACCTTCTGACACAAAA

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**FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67300
><subunit 1 of 1, 172 aa, 1 stop
><MW: 19206, pI: 5.36, NX(S/T): 1
METRPRLGATCLLGFSFLLLVISSDGHNGLGKGFGDHIHWRTLEDGKKEAAASGLPLMVI
IHKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEPPKDEDFSPDGGYIPRILFLDP
SGKVHPEIINENGNP SYKYFYVSAEQVVQGMKEAQRRLTGDAFRKKHLEDEL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-23

**Thioredoxin family proteins:**

Amino acids 58-75

**N-myristoylation sites:**

Amino acids 29-35;67-73;150-156

**Amidation site:**

Amino acid 45-49

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**FIGURE 195**

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTGGATTGAAAGT  
TGAGAGCAGC**ATG**TTTTGCCCCTGAAACTCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGGCCTGAATG  
ACTTGAATGTTTTCCCCGCTGAGCTAACAGTCCATGTGGGTGATTGAGCTCTGATGGGATGTGTTTTCCAGAGC  
ACAGAAGACAAATGTATATTCAAGATAGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCT  
ATACTATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGGACATCTTAT  
GCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGCCTC  
AAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCCCAAGAGCTCATGGT  
CCATGTGGGTGGATTGATTGATGAGATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAAT  
GGATATTTTTCAGGACGGCGCGCAAAGGAGGAGATTGTATTTTCGTTACTACCACAAACTCAGGATGTCTGTGGAG  
TACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCAT  
CATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTC  
AGAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTG  
GTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTGAT  
ATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGA  
CTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATA  
ATTGTACGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGT  
TTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGC  
AAGCCTTT**TG**AGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTCTCTGGGC  
CACTCTACCAAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAG  
ATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATG  
GACTTGGCCTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGAT  
CAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAAACCAACCCAAATCAA

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**FIGURE 196**

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCI FKIDWTLSPGEHAKDEYVLYYY  
SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTICEIRLKGESQVFKKAVVLHVLPEEPKELMVHVG  
GLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLO  
GVRES DGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLPVLLILIV  
KKT CGNKSSVNSTVLVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPEKSEATYMTMHPVWPS  
LRSDRNNSLEKKSGGGMPKTQQAF

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**FIGURE 197**

CGCCATGCCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG  
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTGCGGGCGGCCGGGACCACGGGGACTGGGA  
CGAGGCCTCCCGGCTGCCGCCGCTACCACCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCG  
TGACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGC  
CGGCCCTTCGCCGACGTCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCC  
CTATTTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTA  
CACTGACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTGATCCACAAAGT  
CCCCTTTGTGTTACATAATGCTGTCAGGAAGTGTGACCAAGGTGAATGAAACAGAAATGGA  
TATTGCAAAGCATTTCGTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATA  
ATTGGTTCCTTGCTAAGTTGAATATAACCAATATCTGGGTCCTGGACTACTTTGGTGGACCA  
AAAATCGTGACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAAT  
TTAGCAAACTTATGAAGTTTCTTAAAGTGGCTCATAACACTTAAAAGGCTTAATGTTTCT  
CTGGAAAGCGTCCCAGAATATTAGCCAGTTTTCTGTC

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**FIGURE 198**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSLDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPEMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ
```

**Important features of the protein:****Transmembrane domain:**

Amino acids  
11-29

**N-glycosylation sites:**

Amino acids  
160-164;193-197;216-220

**N-myristoylation sites:**

Amino acids  
3-9;7-13;69-75;97-103

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**FIGURE 199**

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGGGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGCTGGGTGGGGGTTGCTGTGCTGCACCT  
GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT  
GCCATCTCTCGGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTCTTTTGAAGGATATTTAAAATTCATTT  
GAAAAGTGAAGCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC  
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCTCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGTCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTACACTCACATTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA

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**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736  
><subunit 1 of 1, 220 aa, 1 stop  
><MW: 23292, pI: 8.43, NX(S/T): 0  
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM  
QCKVYDSSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAOQKREL GASLYLGWAASGLLLLGGGLLCCTCP  
SGGSQGPHSHYMARYSTSAPAI SRGPSEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186



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**FIGURE 201**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGTCTCCTTCTGCTC  
TGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAAAAAAGTGGACTGCAGCATTTA  
CAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACATACCTACCAGTTTGTGGTTCTGACTACATCACCT  
ATGGGAATGAATGTCACCTTGTGTACCGAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGT  
TGCTAAATTCTCCATGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGAC  
TGAGTTTCTTTCAGTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAATGGA  
GAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTTAAACACGTCAATAA  
AAAAATAATCTCCCAGA

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## **FIGURE 202**

MKITGGLLLLCTVVYFCSSSEAAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNECHLCTESLKSN  
GRVQFLHDGSC

**Important features:**

**Signal peptide:**

amino acids 1-19

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**FIGURE 203**

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGGCTGCGGCGCTG  
CTCTCGTCGCTTGC GCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCTCGTCGCTCAGCCCCCTATTTCCGG  
CACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGTGCGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGC  
TGCTGGAGGGGACCTGCACCCCGGTGCAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAA  
CAGATCCGCAAGCTGAGGCAGCTGCACGGGTTGCTGCAGGCCCGGGTCCAGGGATGGCGGGGCTAGTAGTAC  
CGGCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGCTAG  
TAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGGCCCTTTTCAGCCGT  
GAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCATGGATAGCAGCGCCGCCTTCCTGCA  
GGGGCTGTGGCAGCACTACCACCCTGGCTTGCCGCCGCCGGACGTCGAGATATGGAGTTTGGACCTCCAACAG  
TTAATGATAAACTAATGAGATTTTTTGATCACTGTGAGAAGTTTTAACTGAAGTAGAAAAAATGCTACAGCT  
CTTTATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCA  
AGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTACCTGTTTCACTTGGCAATTA  
AAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAGAATATTTAAATGATCTG  
AAACAATATTGAAAAGAGGATATGGGTATACTATTAACAGTCGATCCAGCTGCACCTTGTTCAGGATATCTT  
TCAGCACTTGGACAAAGCAGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCTCCAGTTTG  
GTCATGCAGAGACTCTTCTTCCACTGCTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTAC  
AATTACAAAAACAAATGCATCGGAAGTTCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGT  
GCTTTTACCCTGTGAAAATGCTAAGACTCCTAAGAACAATTCGAGTGCAGATGTTATTAATGAAAAGGTGT  
TACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAG  
AGTTGTCAAACCAAGTGAAGAATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACCTATGAGTAACTGAAGA  
ACATTTTTTAATTTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAG  
GAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATG  
AAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGCC  
CTGCAAATGTTTACAGAAATGAAATCTTCTACTTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTT  
ATAATAACACTTGAAAAGTGCTGGAGTAACAAATATCTCAGTTGGACCATCCTTAACTTGATTGAAGTGTCTA  
GGAACCTTTACAGATTGTTCTGCAGTTCTCTCTTCTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATCAG  
GAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAAC  
AGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAATATTTTGGTATTTAT  
TTATGAAATATTTGAACATTTTTTCAATAATTCCTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAATTA  
TTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACT  
TTTTTCATTCTGTCACTTGGCTTCGATTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTTGTTGATTT  
TTCTTTCTTTCTTTGTAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAATAAAGAAAATTC  
TTGTGACTTTAAAAA

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**FIGURE 204**

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPLYFGTKTRYEDVNPVLLSGPEAPWRDPELL  
EGTCTPVQLVALIRHGTRYPTVKQIRKLRLHGLLQARGSRDGGASSTGSRDLGAALADWPLWYADWMDGQOLVE  
KGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMDSSAAFLQGLWQHYPGLPPPDVADMEFGPPTVN  
DKLMRFFDHCEKFLTEVEKNATALYHVEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCDFDLAIKG  
VKSPWCDVFDIDDAKVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGH  
AETLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEKVL P  
LAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

**Important features:****Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

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**FIGURE 205**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**  
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA  
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA  
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC  
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
**TGGTAGA**AAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA  
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 206**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

&gt;&lt;subunit 1 of 1, 188 aa, 1 stop

&gt;&lt;MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRINDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDनावDNDsf  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW**Signal peptide:**

amino acids 1-20

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**FIGURE 207**

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACCTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTGCTTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

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**FIGURE 208**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

&gt;&lt;subunit 1 of 1, 178 aa, 1 stop

&gt;&lt;MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK

LGDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISS

AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22



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**FIGURE 209**

GGAGAATEGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGTGGTCTGTCTGCTCCTGGCATGCCCT  
GCCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCTGTGCGAGGCCGGCAGGT  
GGGCGTGAAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTG  
ACCGGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGC  
CTACAAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCTCAACGGAAAAACAGCAGATCTTCTCCGTTTCAGA  
GGACTGCCCTGGTCCCTCAACGTCTATAGCCAGCTGAGGTCCCCGCAGGGTCCGGTAGGCCGGTTCATGGTATGGG  
TCCATGGAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTG  
GTCGTGGTTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAA  
CCAGGGCTTCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCA  
ACTGTGTCACTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCA  
GGGCTGTTCCACAGAGCCATCACACAGATGGGGTTCATACACCCCCAGGGATCATCGACTCTCACCCCTGGCC  
CCTAGCTCAGAAAAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGC  
AGAAAGAAGGAGAAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACT  
GTCTTCCCCAAAAGCCCCAAGGAACCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCCTCATGGGTGTCAA  
CAACCATGAGTTCAGCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGG  
ACATGCTGGCCATCTCAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCACCGTTCATAGAT  
GAATACCTAGGAAGCAACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTTCAT  
CAATGTTCCCACCGTCAGTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCTATGAGTTCAGC  
ATCGACCCAGTCTTTTTGCGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTTGTG  
TTCGGAGGTCCCTTCCTCATGGACGAGAGCTCCCGCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCT  
AAGCCTCACCATGATGGCCAGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTT  
GGCCCCAATTCAACCAGGCGGAACAATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAGTTTCAGGGAG  
GCCTGGATGCAGTCTGGTCAGAGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAA  
GGCCCAGGAGGACCTCGAGGCCAGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAG  
TCCCAGCACGGCAGCCCGCCTCTCCCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCT  
GTGACTGGAGTTATGCTCTTTTGAATGTCAAAAGCCGCTCCACCTCTGGGGCATTGTACAAGTTCTTCCC  
TCTCCCTGAAGTGCCTTTCTGCTTTCTTCTGCTGGTAGGTTCTAGCACATTCTCTAGCTTCTTGGAGGACTCAC  
TCCCCAGGAAGCCTTCCCTGCCTTCTCTGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCC  
GAGGCTAGCACCGTGTCTGTGTCTGTCTCCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCAC  
TCTGTGGGAATGGCAGCTGCTGAACCTGAACCCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGAC  
ATTGTCCACCCTGGCCAGAAGGGTGCATGCCAATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGG  
GATCCAGCCTAGAGCAGACCTTAGCCCTGACTAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGC  
TGCCCACTCCTGGCCCCCTGCACAAGACAACAGAATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTCAC  
CAATTCAGCCCCCTGACCCTCAGGACGCTGGATGCCAGCTCCCAGCCCCAGTGCCCGGTCTCCTCCTTCCCT  
GGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAGAGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGG  
CATCTGGACCAGGGCATCCGTCGGGCTATTGTACAGAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGG  
TGAAAAGCACCAAGAGGTTTTTCAAGTGAAGTGAAGGTGACAGTGTGCTGGCAGCCCTCAGGCCCTCGCTTG  
CTCTCCCTGCCGCTCTGCCTGGGCTCCCACTTTGGCAGCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGT  
AGGAGCCCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCTCCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGG  
CGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAGAGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGG  
CCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCTTAGCACCTGGGCCAGCAGCTGCTGTGCTCGATT  
TCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGAGGGCTCGGGACCTGCAGCCCTCCATGCCTGACCCTCCCC  
CACCCCCCTGGGCTCCTGTGCGGCCGGAGCCTCCCCAAGGAGCGCCGCCCTGCTCCACAGCGCCAGTCCC  
ATCGACCACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGACTGGCAGGCAGCTCCACCTGCTGCCCCAGT  
GCTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGGGGACTTGAGAACTTTATGTCTAGCTAA  
GGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCTGTGT  
CTAGCTAGTGTTTGTGAATGCACCAATCCACTCTGTATCTGTGCTACTCTGGTGGGGACTTGAGAACTTT  
GTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCTTTGTGTCTAGCTCAGGGATCGTAAAC  
GCACCAATCAGCACCTGTCAAAACAGACCACTTGACTCTCTGTAAATGGACCAATCAGCAGGATGTGGGTGG  
GGCAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCCCCCTCGGGTCCCCCTCCACGCCGT  
GGAAGCTTTGTTCTTTTCGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

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## FIGURE 210

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGKGTDRLVNVFLGIPFAQPPLGPDR  
FSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLVNLVYSPA EVPAGSGRPVMVWVH  
GGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFFSTGDEHAPGNQGF LDVVAALRWQENIAPFGGDLNC  
VTVFGGSAGGSIISGLVLS PVAAGLFHRAITQSGVITTPGIIDSHPWPLAQK IANTLACSSSSPAEMVQCLOQK  
EGEELVLSKKLKNTIYPLTVDGTVPKSPKELLKEKPFHSVPFLMGVNNHEFSWLIPRGWGLLDTMEQMSREDM  
LAISTPVLTSLDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEFOHR  
PSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMMAQWTHFARTGDPNSKALPPWP  
QFNQAEQYLEINPVPRAGQKFREAWMQFWSETLP SKIQQWHQKQKNRKAQEDL

**Important features:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 226-245

**N-glycosylation site.**

amino acids 105-109

**N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161, 162-168, 217-223,  
227-233, 228-234, 232-238, 262-268, 357-363, 461-467

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**Carboxylesterases type-B serine active site.**

amino acids 216-232

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**FIGURE 211**

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACAC  
CATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGGTGCAGAGTCTCAGTTGCCC  
GGGAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTG  
GTTTCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAG  
GGTTTTCTGCCAGGATGGAAATGTTAGGTGCTTCTGTGTCTGCGCTGTTCAATTCAGTAGCC  
ACCAGCCACCTGTGGCCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGT  
ATTTTTCTCATTTATTTATTAATTTTTTAAGTATAGTTGTACATATTTGGGGGTACATGTGA  
TATTTGGATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACA  
TCAAACATTTATTTTTTTATTTCTTTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGC  
AGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTC  
CACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTT  
TAGTAGAGACGGGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACCTCCTGGCCTCAAACAAT  
CCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAA  
ACATTTATCTTTTCTTTGTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAACTGTC  
ATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTAC  
CAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCA  
TTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCA  
ATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATG  
TTGCTGCAAATGACAGGATTTCTGTTCTTAATTTCAATTAAAATAACCACACATGGCAAAAA

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## **FIGURE 212**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPLVSC  
QPVKGHGTLGESPMPEKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

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**FIGURE 213**

AGGGCCCGCGGGTGGAGAGAGCGACGCCCGAGGGGATGGCGGCAGCGTCCCGGAGCGCCTCT  
GGCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGGCTCCGGCGTCTT  
CCAGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGGCGTACTGGCCAGTGGGCGGCCTTGCG  
AGCCCGGCTGCCGGACTTTCTTCCGCGTCTGCCTTAAGCACTTCCAGGCGGTGCTCTCGCCC  
GGACCCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGCTGTCCG  
GGACGACAGTAGCGGCGGGGGCGCAACCCTCTCCAACTGCCCTTCAATTTACCTGGCCGG  
GTACCTTCTCGCTCATCATCGAAGCTTGGCACGCGCCAGGAGACGACCTGCGGCCAGAGGCC  
TTGCCACCAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGGTGAGAA  
CTGGTTATTGGATGAGCAAACCAGCACCCCTCACAAGGCTGCGCTACTCTTACCGGGTCACTCT  
GCAGTGACAACACTACTATGGAGACAACCTGCTCCCGCCTGTGCAAGAAGCGCAATGACCACTTC  
GGCCACTATGTGTGCCAGCCAGATGGCAACTTGTCTGCTGCGCGGTTGGACTGGGGAATA  
TTGCCAACAGCCTATCTGTCTTTCGGGCTGTCAACAGAATGGCTACTGCAGCAAGCCAG  
CAGAGTGCCTCTGCCGCCAGGCTGGCAGGGCCGGCTGTGTAACGAATGCATCCCCACAAT  
GGCTGTGCGCCACGGCACCTGCAGCACTCCCTGGCAATGTACTTGTGATGAGGGCTGGGGAGG  
CCTGTTTTGTGACCAAGATCTCAACTACTGCACCCACCACTCCCCATGCAAGAATGGGGCAA  
CGTGCTCCAACAGTGGGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTG  
GACTGTGAGCTGGAGCTCAGCGAGTGTGACAGCAACCCCTGTGCGCAATGGAGGCAGCTGTAA  
GGACCAGGAGGATGGCTACCACTGCCTGTGTCTCCGGGCTACTATGGCCTGCACTGTGAAC  
ACAGCACCTTGAGCTGCGCCGACTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAAC  
CAGGGGGCCAACACTATGCTTGTGAATGTCCCCCAACTTCACCGGCTCCAACCTGCGAGAAGAA  
AGTGGACAGGTGCACCAGCAACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAA  
GCCGCATGTGCCGCTGCCGTCTTGATTACGGGCACCTACTGTGAACCTCCACGTGAGCGAC  
TGTGCCCCGTAACCCTTGCGCCACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTG  
CACCTGCCCTGCCGGCTTCTTGCCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTG  
CCTCGAGTCCCTGCTTCAACAGGGCCACCTGCTACACCGACCTCTCCACAGACACCTTTGTG  
TGCAACTGCCCTTATGGCTTTGTGGGCAGCCGCTGCGAGTTCCCGGTGGGCTTGCCGCCAG  
CTTCCCCTGGGTGGCCGTCTCGCTGGGTGTGGGGCTGGCAGTGTGCTGGTACTGCTGGGCA  
TGGTGGCAGTGGCTGTGCGGCAGCTGCGGCTTCGACGGCCGACGACGGCAGCAGGGAAGCC  
ATGAACAACCTGTGCGGACTTCCAGAAGGACAACCTGATTCCCTGCCGCCAGCTTAAAAACAC  
AAACCAGAAGAAGGAGCTGGAAGTGGACTGTGGCCTGGACAAGTCCAACCTGTGGCAAACAGC  
AAAACCACACATTGGACTATAATCTGGCCCCAGGGCCCCCTGGGGCGGGGGACCATGCCAGGA  
AAGTTTCCCCACAGTGACAAGAGCTTAGGAGAGAAGGCGCCACTGCGGTTACACAGTGAAAA  
GCCAGAGTGTGCGATATCAGCGATATGCTCCCCAGGGACTCCATGTACCAGTCTGTGTGTT  
TGATATCAGAGGAGAGGAATGAATGTGTGCTTGCACGGAGGTATAAGGCAGGAGCCTACCT  
GGACATCCCTGCTCAGCCCCGCGGCTGGACCTTCCTTCTGCATTGTTTACA

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**FIGURE 214**

MAAASRSASGWALLLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCPEPGCRTFFRVCL  
KHFQAVVSPGPCTFGTVSTPVLGTNSFAVRDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHA  
PGDDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQTSTLTRLRYSYRVICSDNYYGDNCSR  
LCKKRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGR  
LCNECIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATCSNSGQRSYTC  
TCRPGYTGVDCLELSECDNPCRNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCF  
NGGSCRERNQGANACECPPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPSRMCRCPGFTG  
TYCELHVSDCARNPCAHGGTCHDLENGLMCTCPAGFSGRRCEVRTSIDACASSPCFNRTCY  
TDLSTDTFVCNCPYGFVGSRCFPVGLPPSFPWVAVSLGVGLAVLLVLLGMVAVAVRQLRLR  
RPDDGSREAMNNLSDFQKDNLIIPAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPG  
PLGRGTMFGKFPKSLGEKAPLRHLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIA  
TEV

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 530-552

**N-glycosylation sites.**

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

**Glycosaminoglycan attachment site.**

amino acids 96-100

**Tyrosine kinase phosphorylation site.**

amino acids 340-347

**N-myristoylation sites.**amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,  
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

**Aspartic acid and asparagine hydroxylation site.**

amino acids 339-351

**EGF-like domain cysteine pattern signature.**amino acids 173-185, 206-218, 239-251, 270-282, 310-322,  
348-360, 388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394,  
411-432, 449-470

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**FIGURE 215**

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCCTACCTGCAGCCGCCGCCACG  
GCACGGCAGCCACCATGGCGCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTTC  
GCCAGAAGTTTGAGTATCACTACTCCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGC  
CTATCTGCCATGCAAATTTACGCTTAGTCCCGAAGACCAGGGACCGCTGGACATCGAGTGGC  
TGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTTATATTCTGGAGACAAA  
ATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTCAA  
ATCTGGTGATGCATCAATAAATGTAACGAATTTACAACGTGTCAGATATTGGCACATATCAGT  
GCAAAGTGAAAAAAGCTCCTGGTGTGCAAATAAGAAGATTTCATCTGGTAGTTCTTGTTAAG  
CCTTCAGGTGCGAGATGTTACGTTGATGGATCTGAAGAAATTGGAAGTGACTTTAAGATAAA  
ATGTGAACCAAAAGAAGGTTCACTTCCATTACAGTATGAGTGGCAAAAATTGTCTGACTCAC  
AGAAAATGCCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTATATCTGTAAAAAATGCC  
TCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATCAGTG  
CCTGTTGCGTCTAAACGTTGTCCCTCCTTCAAATAAAGCTGGACTAATTGCAGGAGCCATTA  
TAGGAACTTTGCTTGTCTAGCGCTCATTGGTCTTATCATCTTTTGCTGTGTAAGAGCGC  
AGAGAAGAAAAATATGAAAAGGAAGTTCATCACGATATCAGGGAAGATGTGCCACCTCCAAA  
GAGCCGTACGTCCACTGCCAGAAGCTACATCGGCAGTAATCATTTCATCCCTGGGGTCCATGT  
CTCCTTCCAACATGGAAGGATATTCCAAGACTCAGTATAACCAAGTACCAAGTGAAGACTTT  
GAACGCACTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCCTTACAAGACTGA  
TGGAATTACAGTTGTATTAAATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTT  
TATTTTAGGCCTCTAGTAAAGACTTAAATGTTTTTTAAAAAAGCACAAGGCACAGAGATTA  
GAGCAGCTGTAAGAACACATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCAT  
GTCAAAATTAGTACGAGCCAAATTCCTTGTAAAAAACCCCTATGTATAGTGACACTGATAGT  
TAAAAGATGTTTTATTATATTTTCAATAACTACCCTAACCAAAATTTTAACTTTTCATATGC  
ATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAAAGGAAATT  
TTAAAATTCCTACGTTCTGTTAATGTTTTTGCTATTTAGTTAAATACATTGAAGGGAAATA  
CCCGTTCCTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTCATGCCTCAAACATTTT  
TTTATTTGCAACTACATGATTTTACACAATTCCTTTAAACAACGACATAAAATAGATTTTCT  
TGTATATAAATAACTTACATACGCTCCATAAAGTAAATTCCTCAAAGGTGCTAGAACAATCG  
TCCACTTCTACAGTGTTCTCGTATCCAACAGAGTTGATGCACAATATATAAATACTCAAGTC  
CAATATTAAAACTTAGGCACTTGACTAACTTTAATAAAATTTCTCAAACATATCAATATC  
TAAAGTGCATATATTTTTTAAGAAAGATTATTCTCAATAACTTCTATAAAAAATAAGTTTGAT  
GGTTTGGCCCATCTAACTTCACTACTATTAGTAAGAAGCTTTTAACTTTTAAATGTGTAGTAAG  
GTTTATTCTACCTTTTTCTCAACATGACACCAACACAATCAAAAACGAAGTTAGTGAGGTGC  
TAACATGTGAGGATTAATCCAGTGATTCCGGTCACAATGCATTCCAGGAGGAGGTACCCATG  
TCACTGGAATTGGGCGATATGGTTTATTTTTTCTTCCCTGATTTGGATAACCAATGGAACA  
GGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTCTGGCTTTTTTCTGGGCAA  
AGGGTGCCACATTGGAAGAGGTGGAAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT  
TAAGTTAATTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCATTAAAGACAAAGTT  
ACCCACAACACTGAGATCACATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAAAA  
ACCTCATGTGTAATAGGCGTATAATGTATAACAGGTGACCAATGTTTTCTGAATGCATAAAG  
AAATGAATAAACTCAAACACAGTACTTCCTAAACAACCTTCAACCAAAAAAGACCAAAACATG  
GAACGAATGGAAGCTTGTAAGGACATGCTTGTTTTAGTCCAGTGGTTTCCACAGCTGGCTAA  
GCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCCTTAG  
CAAACATAATGCAGAAACAGAAAATCAACTACCGCATGTTCTCACTTATAAGTGGGAGGTAAT  
GATAAGAACTTATGAACACAAAGAAGGAAACAATAGACATTGGAGTCTATTTGAGAGGGGAG  
GGTGGGAGAAGGAAAAGGAGCAGAAAAGATAACTATTGAGTACTGCCTTCACACCTGGGTGA  
TGAAATAATATGTACAACAAATCCCTGTGACACATGTTTACCTATGGAACAAACCTTCATGT  
GTATCCCTAAACCTAAAAATAAAAGTTAAAAAARAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361  
><subunit 1 of 1, 352 aa, 1 stop  
><MW: 38938, pI: 7.86, NX(S/T): 3  
MALLLCFVLLCGVVDFAFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA  
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTLNLQLSDIGTYQCKVKK  
APGVANKKIHLVVLVKPSGARCVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT  
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL  
ALALIGLIIFFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM  
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

**Signal sequence.**

amino acids 1-19

**Transmembrane domain:**

amino acids 236-257

**N-glycosylation sites.**

amino acids 106-110, 201-205, 298-302

**Tyrosine kinase phosphorylation sites.**

amino acids 31-39, 78-85, 262-270

**N-myristoylation sites.**amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302**Myelin P0 protein.**

amino acids 96-125



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**FIGURE 217**

GATGGCGCAGCCACAGCTTCTGTGAGATTCTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
AAACAAGTTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
GTTCCAGGCCCTTACCTGCTGGGCACCTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC  
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCC  
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC  
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC  
TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT  
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAACACCACCTCTCTTTACT  
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAAATATCTT  
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT  
ATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
AGCAGGTGATGTATTTTTTATACAGTAAAAAATAACCTTGTAATTCAGAAAGAGTGGCT  
AGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT  
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
CCAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 218**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGN  
IDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSTLT  
IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAQAVVKALGELDILLQWMEETE

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**FIGURE 219**

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCC  
GCGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCTGAGCCTCGGGCTCCGGCCCGGAC  
CTGCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGAT  
GGCTTTAAAAGTGCTACTAGAACAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCT  
ATTTGTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGG  
TCTGGAAACTGTGTTCCCTGCAACAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGG  
CTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACT  
GGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTTCAAGAGGCA  
AATTGTTTACGCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGAC  
GAACTTGTGCGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCCTCCTCCTCCTTACG  
AACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGG  
GACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGTGCTGGCCCTGCTCAT  
CCTCTGTGTCTATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGT  
CGCAGGACATTCAGTACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAA  
TATGCCCACAGAGCCTGCTGCCAGTGCCGCGCTGACTCAGTGCAGACCTGCGGGCCGGTGCG  
CTTGCTCCCATCCATGTGCTGTGAGGAGGCGCTGAGCCCAACCCGGCGACTCTTGTTGTG  
GGGTGCATTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCG  
ACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGAT  
GCAGAATCCCATGGGTGGTGACAACATCTTTTTTGTGACTCTTATCCTGAACTCACTGGAG  
AAGACATTCATTCTCTCAATCCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGT  
CAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTCTCATCTGAAAACCTTTACAGCAGCTAC  
TGATTTATCTAGATATAACAACACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTA  
TGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTC  
CAGGAAGCTTAAAGAACCTGCTTCTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTA  
CTCCTTTGTTAGGCTTATGGACTGAGCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATA  
AATCTGAACCAAACCTGACGGCATTGGAAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGC  
TGTAAGCTGAAACCTCAATGAATAACAAGAAAGACTCCAGGCCGACTCATGATACTCTGCA  
TCTTCTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACTGATGGGTTGAGCT  
GGCAGCCTATGAGATTGTGGACATATAACAAGAAACAGAAATGCCCTCATGCTTATTTTCAT  
GGTGATTGTGGTTTTACAAGACTGAAGACCCAGAGTATACTTTTTCTTTCCAGAAATAATTT  
CATACCGCCTATGAAATATCAGATAAATTACCTTAGCTTTTATGTAGAATGGGTTCAAAGT  
GAGTGTCTTATTTGAGAAGGACACTTTTTCATCATCTAAACTGATTGCGATAGGTGGTTAG  
AATGGCCCTCATATTGCCTGCCTAAATCTTGGGTTTATTAGATGAAGTTTACTGAATCAGAG  
GAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCCACACTTCTGACCTCAGCCTCGGTCTC  
ATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTAGGGAATGTGGTTCGAGAAAGGGCAGC  
CCATTGCCCAGAAATTAACACATATTGTAGAGACTTGTATGCAAAGGTTGGCATATTTATATG  
AAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCCTCTGCCTGAGCTTAGAAGGTTAT  
AGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTGCATTGTATCTTATACTAAAGGC  
TTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGTAGCCTTCCGTGAGAACACACC  
ACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTTGGATGAAGCAGCTGTAAGT  
CCCTAGTGTAGTTTGACCAGGACATTGTGCTGCTCCTTCCAATTGTGTAAGATTAGTTAGCA  
CATCATCTCCTACTTTAGCCATCCGGTGTGTTGATTAAAGAGGACGGTGCTTCTTTCTATTAA  
AGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAGCTAAGACAGAAATTAAC  
CCCGTTTCAAGTCAAAAGCAGGGAATGGTTTCACTTTTACTCTTAATCTTTATGCCCTGGAGAAGA  
CCTACTTGAACAGGGCATATTTTTTTAGACTTCTGAACATCAGTATGTTTCGAGGGTACTATGA  
TATTTTGGTTTGGAAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTTAACTGAATATTAA  
AATGTATCTGTCTTTCCT

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## FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVTCLHRFKEDWGFQKCKPCLDCAVVNRFOKANCSATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDP PPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILLCVIYCKRQFMEKKPSWSLSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLLPSMCCEEACSPNPATLGC GVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

### Important features of the protein:

#### Signal peptide:

Amino acids  
1-25

#### Transmembrane domain:

Amino acids  
169-192

#### N-glycosylation sites:

Amino acids  
105-109;214-218;319-323;350-354;368-372;379-383

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids  
200-204;238-242

#### Tyrosine kinase phosphorylation site:

Amino acids  
207-214

#### N-myristoylation sites:

Amino acids  
55-61;215-221;270-276

#### Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids  
259-270

#### TNFR/NGFR family cysteine-rich region proteins:

Amino acids  
89-96

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**FIGURE 221**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTT  
TAATCCAGGATCCTGTCCTTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACA  
AGTTTGTCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAAC  
TCCTGTGGGCACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTG  
GGCCTGCCGTGGAAGGGAGGTCTGTCCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGAT  
CCTGCTGATCTATGCCTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGG  
CTCGTTACCTCCCTGCCACAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGAC  
TACTATGCCTACAGACTGGGGCACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGAC  
TGTATTCTCAATGGAGCTACTGCTGGGGAGAAGTGGTGGGAAATTTGAAGACGACATTG  
ACAACTGCCATTTCCAAGAAAGCACAGAGCTGAACAATACTTTCACCTGCTTCTTCACCATC  
AGCACCAGGCCCTGGATGACTCAGTTCAGCCTCCTGAACAAGACCTGCTTGGAGGGATTCCA  
CTGAGTGAAACCCACTCACAGGCTTGTCCATGTGCTGCTCCCACATTCCGTGGACATCAGCA  
CTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCTTTGGACTTGTTTGTATCCTATTTTG  
CATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAAATCCACACATCTTGAGCCTAATCATGT  
AGTGTAGATCATTAACATCAGCATTTTAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 222**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQS  
KDYAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFF  
TISTRPWMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

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**FIGURE 223**

AATCGGCTGATTCTGCATCTGGAACTGCCTTCATCTTGAAAGAAAAGCTCCAGGTCCCT  
TCTCCAGCCACCCAGCCCCAAGATGGTGATGCTGCTGCTGCTGCTTTCCGCACTGGCTGG  
CCTCTTCGGTGCGGCAGAGGGACAAGCATTTCATCTTGGGAAGTGCCCCAATCCTCCGGT  
GCAGGAGAATTTTGACGTGAATAAGTATCTCGGAAGATGGTACGAAATTGAGAAGATCCC  
AACAACCTTTGAGAATGGACGCTGCATCCAGGCCAACTACTCACTAATGGAAAACGGAAA  
GATCAAAGTGTTAAACCAGGAGTTGAGAGCTGATGGAAGTGTGAATCAAATCGAAGGTGA  
AGCCACCCAGTTAACCTCACAGAGCCTGCCAAGCTGGAAGTTAAGTTTCCTGGTTTAT  
GCCATCGGCACCGTACTGGATCCTGGCCACCGACTATGAGAAGTATGCCCTCGTGTATTC  
CTGTACCTGCATCATCCAACTTTTTACGTGGATTTTGCTTGGATCTTGGCAAGAAACCC  
TAATCTCCCTCCAGAAACAGTGGACTCTCTAAAAAATATCCTGACTTCTAATAACATTGA  
TGTCAGAGAAATGACGGTCACAGACCAGGTGAACTGCCCCAAGCTCTCGTAAACAGGTTT  
TACAGGGAGGCTGCACCCACTCCATGTTACTTCTGCTTCGCTTTCCCCTACCCACCCCC  
CCCCATAAAGACAAACCAATCAACCACGACAAAGGAAGTTGACCTGAACATGTAACCAT  
GCCCTACCCTGTTACCTTGCTAGCTGCAAAATAAACTTGTGCTGACCTGCTGTGCTCGC  
AAAAAA

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**FIGURE 224**

MVMLLLLLSALAGLFGAAEGQAFHLGKCPNPPVQENFDVNKYLGRWYEIEKIPTTFENG  
RCIQANYSLMENGKIKVLNQELRADGTVNQIEGEATPVNLTEPAKLEVKFSWFMPSAPY  
WILATDYENYALVYSCTCIIQLFHVDFAWILARNPNLPPETVDSLKNILTSNNIDVKKM  
TVTDQVNCPKLS

Signal sequence  
1-16

N-glycosylation site.

65-68  
98-101

cAMP- and cGMP-dependent protein kinase phosphorylation site.

175-178

N-myristoylation site.

13-18  
16-21

Lipocalin proteins.

36-47  
120-130

Lipocalin / cytosolic fatty-acid binding proteins

41-185



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**FIGURE 225**

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTG  
CCTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGG  
GCGTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAA  
TTCAGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCA  
AAAAAGGACTCACCTCCCAAAAATTCCTGTAAGGTTGATGAGCTTTCACTCTACTCAGTTCC  
TGAGGGTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGC  
TCCGACACTATTGCGAGCCATACACAACCTGGTGTGTCAGGAAACGTA TCCCAAACTAAGCCC  
AAGATGCAAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCC  
TGGATTTTTTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTA  
GAGGTTCAAAAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTC  
TATTATCCACAACAAGCCATCGTGTTTGCCAGGTCAGTGGGGAGAGATTATATGACTGGGG  
TTTACGAGGATATATAGTCATAGAAGATTTGTGGAAGGAGAACTTTCAAAGCCAGGAAATG  
TGAAGAATTCACCTGGAAC TAAGTAGAAAACCTCCATGCTCTGCCATCTTAATCAGTTATAGG  
TAAACATTGGAACTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAG  
TATTGAATGTATTAAATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTT  
CTGTGAAATCATCCTACAAGCAAACCTGGAATCCCTTCACCTAGAGATAATGTACAAG  
CCTTAGAACTCCTCATTCTCATGTTGCTATTTATGTACCTAATTAAAACCCAAGTTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 226**

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEE  
SISQLRHYPEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAAPPGFFPRLGVIGFAGLIG  
LLLARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQ  
KPGNVKNSPGTK

**Important features:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 111-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 36-44

**N-myristoylation sites:**

Amino acids 124-130;144-150;189-195

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**FIGURE 227**

CACCGGAGGGCACGCAGCTGACGGAGCTGCGCTGCGTTTCGCTCGCGCCCTCC  
ACTGGAGCTGTTTCGCGCCTCCCGGCTCCCACCGCAGCCCACCCGGCAGAGGAGTCGCTACCA  
GCGCCAGTGCGCTCTGTCAGTCCGCAAACCTCCTTGCCGCCCGCCCCGGGCTGGGCACCAAA  
TACCAGGCTACCATGGTCTACAAGACTCTCTTCGCTCTTTGCATCTTAAGTGCAGGATGGAG  
GGTACAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCAC  
CGACCACCATCTGGACTAGCTCTCCACAAAACACTGATGCAGACACTGCCTCCCCATCCAAC  
GGCACTCACAACAACCTCGGTGCTCCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAA  
GAACATTTCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCCAGGTTTCAATTGGGAAGGCA  
CAAACACAGACCCCTCACCTTCTGGGTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACC  
ACGTTGGAGGAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTGCGAGTC  
CGCTGCTGAGCCTCCACACTCATCTCCCTCAAGCTCCAGCCTCATCACCTCATCCCTAT  
CAACCTCACCACCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACC  
AGCACCCAACCCACTGGAGCTCCAAGTGCACCAGAGTCCCCGACAGAGGAGTCCAGCTCTGA  
CCACACACCCACTTCACATGCCACAGCTGAGCCAGTGCCCCAGGAGAAAACACCCCCAACAA  
CTGTGTCAGGCAAAGTGATGTGTGAGCTCATAGACATGGAGACCACCACCACCTTTCCCAGG  
GTGATCATGCAGGAAGTAGAACATGCATTAAAGTTCAGGCAGCATCGCCGCCATTACCGTGAC  
AGTCATTGCCGTGGTGCTGCTGGTGTTTGGAGTTGCAGCCTACCTAAAAATCAGGCATTTCCT  
CCTATGGAAGACTTTTGGACGACCATGACTACGGGTCTTGGGGAAACTACAACAACCCTCTG  
TACGATGACTCCTAACAATGGAATATGGCCTGGGATGAGGATTAAGTGTCTTTATTTATAA  
GTGCTTATCCAGTAGAATTAATAAGTACCTGATGCGCATTTGAACGACAATCTTAAGCCCTGT  
TTTGTTGGTATGGTTGTTTTTGTTCCTCCCTCTCCTCTGGCTGCTACAACTTCCCCTTTC  
TGGTACAAGAAGAACCATTCTTTAAAGGTGAGTGGAGGCTGATTTCAGCTGAAGTGGGCCA  
GCCTTGCACCAGCCAGGCCAGACCACCATGGTGAAGGCTTCTTTCCCCACTGCAGGACCCAC  
TTTGAGAAGGATCGAGGAGGAGGATTTGGGTGTTTTGTAGGGGTACTTTTCAGGGGAACA  
TTTCATTTGTGTTATTTCTTAACTTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGA  
AAGGAAATGAGCTCTACGAGGATTTACCTTGCATGGGAGAGAGCAGGGTTTTCTCAGATTC  
CTTTTAAATCTCTATTTATCTGGTTGTTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGC  
TGGAAAGCAGCTTCTTAGCTGCCTAATTAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGG  
GGCCAGCAGGTCACGGGGCAGAATCTCTCAGGTTGCTGTGGGATCTCAGTGTGCCCTACCT  
GTTCTCCCCCTCCAGGCCACCTGTCTCTGTAAAGGATGTCTGCTCTGTTCAAAAGGCAGCTGG  
GATCCCAGCCCACAAGTGATCAGCAGAGTTGCATTTCCAAAGAAAAAGGCTATGAGATGAGC  
TGAGTTATAGAGAGAAAGGGAGAGGCATGTACGGTGTGGGGAAGTGGAAGAGAAGCTGGCGG  
GGGAGAAGGAGGCTAACCTGCACTGAGTACTTCATTAGGACAAGTGAGAATCAGCTATTGAT  
AATGGCCAGAGATATCCACAGCTTGGAGGAGCCCAGAGACTGTTTGCTTTATACCCACACAG  
CAACTGGTCCACTGCTTTACTGTCTGTTGGATAATGGCTGTAAAATGTTTAAAAAC

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## FIGURE 228

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHN  
NSVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEE  
HSSGTPEAGVAATLSQSAAPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSTVTSTQP  
TGAPTAPESPTEESSSDHTPTSHATAEPVPQEKTPPTTVSGKVMCELIDMETTTTFPRVIMQ  
EVEHALSSGSIAAITVTVIAVLLVFGVAAYLKIRHSSYGRLDDHDYGSWGNYNPLYDDS

### Important features of the protein:

#### Signal peptide:

amino acids 1-20

#### Transmembrane domain:

amino acids 258-278

#### N-glycosylation sites.

amino acids 58-61, 62-65, 80-83, 176-179

#### Casein kinase II phosphorylation sites.

amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-144, 164-167, 191-194, 195-198, 200-203

#### Tyrosine kinase phosphorylation site.

amino acids 289-296

#### N-myristoylation sites.

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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**FIGURE 229**

CTCCTGCACTAGGCTCTCAGCCAGGGATGATGCGCTGCTGCCGCCGCCGCTGCTGCTGCCGG  
CAACCACCCCATGCCCTGAGGCCGTTGCTGTTGCTGCCCTCGTCCTTTTACCTCCCCTGGC  
AGCAGCTGCAGCGGGCCCAAACCGATGTGACACCATATAACCAGGGCTTCGCCGAGTGTCTCA  
TCCGCTTGGGGGACAGCATGGGCCGCGGAGGCGAGCTGGAGACCATCTGCAGGTCTTGGAAT  
GACTTCCATGCCTGTGCCTCTCAGGTCCTGTCAGGCTGTCCGGAGGAGGCAGCTGCAGTGTG  
GGAATCACTACAGCAAGAAGCTCGCCAGGCCCCCCGTCCGAATAACTTGCACACTCTGTGCG  
GTGCCCCGGTGCATGTTTCGGGAGCGCGGCACAGGCTCCGAAACCAACCAGGAGACGCTGCGG  
GCTACAGCGCCTGCACTCCCCATGGCCCCCTGCGCCCCCACTGCTGGCGGCTGCTCTGGCTCTG  
GCCTACCTCCTGAGGCCTCTGGCCTAGCTTGTTGGGTTGGGTAGCAGCGCCCGTACCTCCAG  
CCCTGCTCTGGCGGTGGTTGTCCAGGCTCTGCAGAGCGCAGCAGGGCTTTTCATTAAAGGTA  
TTTATATTTGTA

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**FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92265
><subunit 1 of 1, 165 aa, 1 stop
><MW: 17786, pI: 8.43, NX(S/T): 0
MMRCCRRRCCCRQPPHALRPLLLLPLVLLPPLAAAAAGPNRCDTIYQGFAECLIRLGDSM
GRGGELETICRSWNDFHACASQVLSGCP EEA AVWESLQQEARQAPRPNNLHTLCGAPVH
VRERGTGSETNQETLRATAPALPMAPAPPLLAALALAYLLRPLA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-35

**Transmembrane domain:**

Amino acids 141-157

**N-myristoylation site:**

Amino acids 127-133

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 77-88

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**FIGURE 231**

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT  
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTGGACAATGAGGCTGGTCACAGCAGCACTG  
TACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA  
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG  
GGAACATTGGCTGCAAGGTTGTTCTTGATTGTAACAACACTACAGACAGAAGATCACCTCCTGG  
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT  
GGATCCAGATGCCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA  
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTGAGGGCCAGGAGTTATCAGCCTAC  
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAAGTTCTTTGTCTATCTTCA  
GGAAGGAAAAGTCATCTCTCTCTTCCCAAGGAAAACAAACTCGAGGCTCTTGGAATAATGG  
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG  
AACTACCAGGACTCACCAACCCTCCAGGCTCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA  
AACCAGGCAGAGAT**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC  
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCTTCTTTTCCAA  
ATTAAAAAAAAAATCATCAA

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**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274  
><subunit 1 of 1, 223 aa, 1 stop  
><MW: 25402, pI: 8.14, NX(S/T): 1  
MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP  
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK  
KGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL  
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 169-173

**Tyrosine kinase phosphorylation site.**

amino acids 59-68

**N-myristoylation sites.**

amino acids 54-60, 83-89, 130-136

**Phosphatidylethanolamine signature.**

amino acids 113-157



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**FIGURE 233**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA  
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC  
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT  
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

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**FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282  
><subunit 1 of 1, 177 aa, 1 stop  
><MW: 20452, pI: 8.00, NX(S/T): 2  
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST  
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ  
RQCHCRQEQATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

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**FIGURE 235**

GCCCCGGGCGGCTGCCCTTGGGTGCTCCCTTCCCTGCCCCGACACCCAGACCGACCTTGACCGC  
CCACCTGGCAGGAGCAGGACAGGACGGCCGGACGCGGCC**ATG**GCCGAGCTCCCGGGGCCCCTT  
TCTCTGCGGGGCCCTGCTAGGCTTCCTGTGCCTGAGTGGGCTGGCCGTGGAGGTGAAGGTAC  
CCACAGAGCCGCTGAGCACGCCCCCTGGGGAAGACAGCCGAGCTGACCTGCACCTACAGCACG  
TCGGTGGGAGACAGCTTCGCCCTGGAGTGGAGCTTTGTGCAGCCTGGGAAACCCATCTCTGA  
GTCCCATCCAATCCTGTACTTCACCAATGGCCATCTGTATCCAAGTGGTTCTAAGTCAAAGC  
GGGTGAGCCTGCTTCAGAACCCCCCACAGTGGGGGTGGCCACACTGAAACTGACTGACGTC  
CACCCCTCAGATACTGGAACCTACCTCTGCCAAGTCAACAACCCACCAGATTCTACACCAA  
TGGGTTGGGGCTAATCAACCTTACTGTGCTGGTTCCCCCAGTAATCCCTTATGCAGTCAGA  
GTGGACAAACCTCTGTGGGAGGCTCTACTGCACTGAGATGCAGCTCTTCCGAGGGGGCTCCT  
AAGCCAGTGTACAACCTGGGTGCGTCTTGGAACCTTTTCCTACACCTTCTCCTGGCAGCATGGT  
TCAAGATGAGGTGTCTGGCCAGCTCATTCTCACCAACCTCTCCCTGACCTCCTCGGGCACCT  
ACCGCTGTGTGGCCACCAACCAGATGGGCAGTGCATCCTGTGAGCTGACCCTCTCTGTGACC  
GAACCCTCCCAAGGCCGAGTGGCCGGAGCTCTGATTGGGGTGCTCCTGGGCGTGCTGTTGCT  
GTCAGTTGCTGCGTTCTGCCTGGTCAGGTTCCAGAAAGAGAGGGGGAAGAAGCCCAAGGAGA  
CATATGGGGGTAGTGACCTTCGGGAGGATGCCATCGCTCCTGGGATCTCTGAGCACACTTGT  
ATGAGGGCTGATTCTAGCAAGGGGTTCTTGAAAGACCCTCGTCTGCCAGCACCGTGACGAC  
CACCAAGTCCAAGCTCCCTATGGTCGTG**TGA**CTTCTCCCGATCCCTGAGGGCGGTGAGGGGG  
AATATCAATAATTAAAGTCTGTGGGTACCCTTNAAAAAAAAAAAAA

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**FIGURE 236**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108760
><subunit 1 of 1, 327 aa, 1 stop
><MW: 34348, pI: 7.88, NX(S/T): 2
MAELPGPFLLCGALLGFLCLSGLADEVKVPTEPLSTPLGKTAELTCTYSTSVGDSFALEWS
FVQPGKPISESHPILYFTNGHLYPTGSKSRVSLQLQNPPTVGVATLKLTDVHPSDTGTYL
CQVNNPPDFYTNGLGLINLTVLVPPSNPLCSQSGQTSVGGSTALRCSSSEGAPKPVYNWV
RLGTFPTPSPGSMVQDEVSGQLILTNLSLTSSGTYRCVATNQMGASCELTLSVTEPSQG
RVAGALIGVLLGVLLLSVAAFLVRFQKERGKKPKETYGGSDLREDAIAPGISEHTCMRA
DSSKGFLERPSSASTVTTTTSKSLPMVV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 242-260

**N-glycosylation sites:**

Amino acids 138-142;206-210

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 90-94

**N-myristoylation sites:**Amino acids 11-17;117-123;159-165;213-219;224-230;244-250;  
248-254**Amidation site:**

Amino acids 270-274

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 218-229

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**FIGURE 237**

GGATGCAGCAGAGAGGAGCAGCTGGAAGCCGTGGCTGCGCTCTCTTCCCTCTGCTGGGCG  
TCCTGTTCTTCCAGGGTGTTTATATCGTCTTTTCCTTGGAGATTCGTGCAGATGCCCATG  
TCCGAGGTTATGTTGGAGAAAAGATCAAGTTGAAATGCACTTTCAAGTCAACTTCAGATG  
TCACTGACAAGCTTACTATAGACTGGACATATCGCCCTCCAGCAGCAGCCACACAGTAT  
CAATATTTTATTATCAGTCTTTCCAGTACCCAACCACAGCAGGCACATTTTCGGGATCGGA  
TTTCCTGGGTTGGAAATGTATACAAAGGGGATGCATCTATAAGTATAAGCAACCCTACCA  
TAAAGGACAATGGGACATTGAGCTGTGCTGTGAAGAATCCCCAGATGTGCACCATAATA  
TTCCCATGACAGAGCTAACAGTCACAGAAAGGGGTTTTGGCACCATGCTTTCCTCTGTGG  
CCCTTCTTTCCATCCTTGCTTTGTGCCCTCAGCCGTGGTGGTTGCTCTGCTGCTGGTGA  
GAATGGGGAGGAAGGCTGCTGGGCTGAAGAAGAGGAGCAGGTCTGGCTATAAGAAGTCAT  
CTATTGAGGTTTCCGATGACACTGATCAGGAGGAGGAAGAGGCGTGTATGGCGAGGCTTT  
GTGTCCGTTGCGCTGAGTGCCTGGATTGAGACTATGAAGAGACATATGATGAAAGTCTG  
TATGACACAAGAAGAGTCACCTAAAGACAGGAACATCCCATTCCACTGGCAGCTAAAGC  
CTGTCAGAGAAAGTGGAGCTGGCCTGGACCATAGCGATGGACAATCCTGGAGATCATCAG  
TAAAGACTTTAGGAACCACTTATTTATTGAATAAATGTTCTTGTTGTATTTATAAACTGT  
TCAGGAAGTCTCATAAGAGACTCATGACTTCCCCTTTCAATGAATTATGCTGTAATTGAA  
TGAAGAAATTCTTTTCTGAGCA

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**FIGURE 238**

MQQRGAAGSRGCALFPLLGVLFQGVYIVFSLEIRADAHVRGYVGEKIKLKCTFKSTSD  
VTDKLTIDWTYRPPSSSHTVSI FHYQSFOYPTTAGTFRDRISWVG NVYKGDASISINP  
TIKDNGETFSCAVKNPPDVHHNIPMTELTVTERGFGTMLSSVALLSILVFVPSAVVVALL  
LVRMGRKAAGLKKRSRSGYKKSSIEVSDDTDQEEEEACMARLCVRCAECLDSDYEETY

**Transmembrane domain**

11-30  
157-177

**N-glycosylation site**

123-127

**cAMP- and cGMP-dependent protein kinase phosphorylation site**

189-193  
197-201

**Tyrosine kinase phosphorylation site**

63-71

**N-myristoylation site**

5-11  
8-14  
124-130  
153-159

**Amidation site**

181-185

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**FIGURE 239**

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCC  
TCGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTCGCCTCTGTT  
TGGGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAACATAAAATTTGAAAGCAAGATTGAAGAGAT  
GGTTGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTT  
TATCAGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAACTGACAAA  
CTCATGATGGACGGCCACGAGGTGACCGTGCGTGGGACAATTTCTTCACGGGCAGGAAGAGAAAACGTGGAGCACTG  
GATCGGACATGAGAACTTCGAGTTGATTAAACCACGACGTGGTGGAGCCCCCTCTACATCGAGGTTGACCAGATAT  
ACCATCTGGCATCTCCAGCCTCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATT  
GGGACATTAAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTA  
TGGAGATCCTGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCT  
ACGATGAAGGCAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAGTGCGAGTG  
GCCAGAATCTTCAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCA  
GGCGCTCCAGGGGGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCAGTACGTACGCGATC  
TAGTGAATGGCCTCGTGGCTCTCATGAACAGCAACGTACAGAGCCCGGTCAACCTGGGGAACCCAGAAGAACAC  
ACAATCCTAGAATTTGCTCAGTTAATTAATAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGC  
CCAGGATGACCCACAGAAAAGAAAACAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCC  
CGCTGGAGGAAGGTTTAAACAAAGCAATTCCTACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTAC  
ATCCCCAAACCAAAGCCTGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTGAACCTCCTCACTTTTAGGACAC  
AAGACTACCATTTGTACACTTGATGGGATGTATTTTGGCTTTTTTTTGTGTGCTTTAAAGAAAGACTTTAACA  
GGTGTGATGAAGAACAACCTGGAATTTTATTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCC  
TCAAAAACTGCAGATTTTGCCTTGCACTTTTGAATCTCTCTTTTATGTAAATAGCGTAGATGCATCTCTG  
CGTATTTTCAAGTTTTTTTATCTTGCTGTGAGAGCATATGTTGTGACTGTCGTTGACAGTTTTATTTACTGGTT  
TCTTTGTGAAGCTGAAAAGGAACATTAAGCGGGACAAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAAT  
AAATGAGTCGTTATACTATGCATAAAGAAAAATCCTAGCAGTATTGTGAGGTGGTGGTGCGCCGGCATTGATTT  
TAGGGCAGATAAAAGAATTCTGTGTGAGAGCTTTATGTTTCTCTTTTAATTGAGGTTTTTCCAAGGTCTACTT  
TTGAGTTGCAAACTTGACTTTGAAATATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTT  
GCTGCGTATCTGGGGCGGGGCAGGTTGGGGGGCACAAAGTTAACATATTCTTGGTTAACCATGGTTAAATATG  
CTATTTTAATAAAATATTGAAACTCA

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**FIGURE 240**

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPL  
REKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMDGHEVTVDNFFTG  
RKRNVHEHWIGHENFELINHADVVEPLYIEVDQIYHLASPSPNYMYPNPIKTLKTNITIGTLNM  
LGLAKRVGARLLLASTSEVYGDPEVHPQSEDYWGHVNPIGPRACYDEGKRVAETMCYAYMKQ  
EGVEVRVARI FNTFGPRMHMNDGRVVSNEFILQALQGEPLTVYSGSGSQTAFQYVSDLVNGLV  
ALMNSNVSSPVNLGNPEEHTILEFAQLIKNLVGSGSEIQFLSEAQDDPQKRKPDIKKAKLML  
GWEPVVPLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

**Important features:****Signal peptide:**

amino acids 1-32

**N-glycosylation site:**

amino acids 316-320

**Tyrosine kinase phosphorylation site:**

amino acids 235-244

**N-myristoylation sites:**

amino acids 35-41, 101-107, 383-389

**Amidation sites:**

amino acids 123-127, 233-237



**FIGURE 241**

GCCCGGTGGAGAATTAGGTGCTGCTGGGAGCTCCTGCCTCCACAGGATTCCAGCTGCAGGG  
 AGCCTCAGGGACTCTGGGCCGCACGGAGTTGGGGGCATTCCCCAGAGAGCGTCGCC**ATGGTC**  
 TGCAGGGAGCAGTTATCAAAGAATCAGGTCAAGTGGGTGTTTGCCGGCATTACCTGTGTGTC  
 TGTGGTGGTCATTGCCGCAATAGTCCTTGCCATCACCTGCGGGCGGCCAGGCTGTGAGCTGG  
 AGGCCTGCAGCCCTGATGCCGACATGCTGGACTACCTGCTGAGCCTGGGCCAGATCAGCCGG  
 CGAGATGCCTTGAGGTCACCTGGTACCACGCAGCCAACAGCAAGAAAGCCATGACAGCTGC  
 CCTGAACAGCAACATCACAGTCCTGGAGGCTGACGTCAATGTAGAAGGGCTCGGCACAGCCA  
 ATGAGACAGGAGTTCCCATCATGGCACACCCCCCACTATCTACAGTGACAACACACTGGAG  
 CAGTGGCTGGACGCTGTGCTGGGCTCTTCCCAAAGGGCATCAAAGTGGACTTCAAGAACAT  
 CAAGGCAGTGGGCCCCCTCCCTGGACCTCCTGCGGCAGCTGACAGAGGAAGGCAAAGTCCGGC  
 GGCCCATATGGATCAACGCTGACATCTTAAAGGGCCCCAACATGCTCATCTCAACTGAGGTC  
 AATGCCACACAGTTCTTGGCCCTGGTCCAGGAGAAGTATCCCAAGGCTACCCTATCTCCAGG  
 CTGGACCACCTTCTACATGTCCACGTCCCCAAACAGGACGTACACCCAAGCCATGGTGGAGA  
 AGATGCACGAGCTGGTGGGAGGAGTGCCCCAGAGGGTCACCTTCCCTGTACGGTCTTCCATG  
 GTGCGGGCTGCCTGGCCCCACTTCAGCTGGCTGCTGAGCCAATCTGAGAGGTACAGCCTGAC  
 GCTGTGGCAGGCTGCCTCGGACCCCATGTCGGTGGAAAGATCTGCTCTACGTCCGGGATAACA  
 CTGCTGTCCACCAAGTCTACTATGACATCTTTGAGCCTCTCCTGTACAGTTCAAGCAGCTG  
 GCCTTGAATGCCACACGGAAACCAATGTACTACACGGGAGGCAGCCTGATCCCTCTTCTCCA  
 GCTGCCTGGGGATGACGGTCTGAATGTGGAGTGGCTGGTTCCTGACGTCCAGGGCAGCGGTA  
 AAACAGCAACAATGACCCTCCCAGACACAGAAGGCATGATCCTGCTGAACACTGGCCTCGAG  
 GGAAGTGTGGCTGAAAACCCCGTGCCCATTTGTTTCACTCTCCAAGTGGCAACATCCTGACGCT  
 GGAGTCCTGCCTGCAGCAGCTGGCCACACATCCCGGACACTGGGGCATCCATTTGCAAATAG  
 TGGAGCCCGCAGCCCTCCGGCCATCCCTGGCCTTGCTGGCACGCCTCTCCAGCCTTGCCCTC  
 TTGCATTGGCCTGTGTGGGTGGGGCCAAAATCTCCACGGGAGTTTTTTCGGTCCCCGGCCA  
 TGTGGCTGGCAGAGAGCTGCTTACAGCTGTGGCTGAGGTCTTCCCCACGTGACTGTGGCAC  
 CAGGCTGGCCTGAGGAGGTGCTGGGCAGTGGCTACAGGGAACAGCTGCTCACAGATATGCTA  
 GAGTTGTGCCAGGGGCTCTGGCAACCTGTGTCCTTCCAGATGCAGGCCATGCTGCTGGGCCA  
 CAGCACAGCTGGAGCCATAGGCAGGCTGCTGGCATCCTCCCCCGGGGCCACCGTCACAGTGGAG  
 CACAACCCAGCTGGGGGCGACTATGCCTCTGTGAGGACAGCATTGCTGGCAGCTAGGGCTGT  
 GGACAGGACCCGAGTCTACTACAGGCTACCCAGGGCTACCACAAGGACTTGCTGGCTCATG  
 TTGGTAGAACT**TGA**GCACCCAGGGGTGGTGGGCCAGCGGACCTCAGGGCGGAGGCTTCCCAC  
 GGGGAGGCAGGAAGAAATAAAGGTCTTTGGCTTTCTCCAGGCCAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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**FIGURE 242**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119514
><subunit 1 of 1, 585 aa, 1 stop
><MW: 64056, pI: 6.58, NX(S/T): 5
MVCREQLSKNQVKWVFAGITCVSVVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG
QISRRDALEVTWYHAANSKKAMTAALNSNITVLEADVNVVEGLGTANETGVPIMAHPTIY
SDNTLEQWLDVAVLGSSQKGIKLDKFNIAVGPISLDLLRQLTEEGKVRPPIWINADILKGP
NMLISTEVNATQFLALVQEKYPKATLSPGWTFYFYMSTSPNRTYTQAMVEKMHVELVGGVPQ
RVTFPVRSSMVRAAWPHFSWLLSQSERYSLLTLWQAASDPMSVEDLLYVRDNTAVHQVYYD
IFEPLLSQFKQLALNATRKPMPYYTGGSLLIPLLQLPGDDGLNVEWLVPDVQGGSGKTATMTL
PDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLESCLOQLATHPGHWGIHLQIVEPAA
LRPSLALLARLSSLGLLHWPVWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHTVAPGW
PEEVLGSGYREQLLTDMLELCQGLWQPVSFQMAMLLGHSTAGAIGRLLASSPRATVTVE
HNPAGGDYASVRTALLAARAVDRTRVYYRLPQGYHKDLLAHVGRN
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 18-37 (Possible type II)

**N-glycosylation sites:**

Amino acids 89-93;106-110;189-193;220-224;315-319

**Tyrosine kinase phosphorylation site:**

Amino acids 65-74

**N-myristoylation sites:**

Amino acids 101-107;351-357;372-378;390-396;444-450;545-551

**Aminotransferases class-V pyridoxal-phosphate attachment site:**

Amino acids 312-330

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**FIGURE 243**

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATGGC  
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC  
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGAC  
AAGTCCAACCTCCAGCAGCCCTATATCACCACCCGACCTTCATGCTGGCTAAGGAGGCTAG  
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA  
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTT  
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG  
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA  
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGT  
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAA  
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC  
CAAAAGGAAGATGGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT  
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA  
TAGATATTTATTGATAACATTTCAATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT  
TTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCATTCCCTTAGGGGAAAAAACCC  
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA  
TAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG  
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC  
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

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**FIGURE 244**

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE  
ASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLEEVLFPPQSDRFQPYMQEVVPFLAR  
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

# INTERNATIONAL SEARCH REPORT

International Application No. **PCT/US 10/17800**

**A. CLASSIFICATION OF SUBJECT MATTER**  
**IPC 7 B01D39/16**

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)  
**IPC 7 B01D**

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

**EPO-Internal**

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 4 215 682 A (DAVIS CHARLES I ET AL) 5 August 1980 (1980-08-05) column 6, line 23 - line 31; figure 4	1,2,7,9
Y	US 5 645 627 A (LIFSHUTZ NORMAN ET AL) 8 July 1997 (1997-07-08) Summary of the invention column 4, paragraph 2 - paragraph 3 column 6, paragraph 2 - paragraph 3	1,2,7,9

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

**\* Special categories of cited documents:**

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*&\* document member of the same patent family

Date of the actual completion of the international search

**10 September 2001**

Date of mailing of the international search report

**18/09/2001**

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
 NL - 2280 HV Rijswijk  
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
 Fax: (+31-70) 340-3016

Authorized officer

**Plaka, T**

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 10/17800

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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		IT 1116822 B	10-02-1986
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		NL 7900855 A	08-08-1979
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